



Cura 468 SEQ list 0705
SEQUENCE LISTING



<110> Guo, Xiaojia
<120> Proteins and Nucleic Acids Encoding Same
<130> 21402-168
<140> 09/981,151
<141> 2001-10-16
<150> 60/241,040
<151> 2000-10-17
<150> 60/241,058
<151> 2000-10-17
<150> 60/241,063
<151> 2000-10-17
<150> 60/241,243
<151> 2000-10-17
<150> 60/242,152
<151> 2000-10-20
<150> 60/242,482
<151> 2000-10-23
<150> 60/242,611
<151> 2000-10-23
<150> 60/242,612
<151> 2000-10-23
<150> 60/242,880
<151> 2000-10-24
<150> 60/242,881
<151> 2000-10-24
<150> 60/259,028
<151> 2000-12-29
<150> 60/269,813
<151> 2001-02-20
<150> 60/286,324
<151> 2001-04-25
<150> 60/294,108
<151> 2001-05-29
<150> 60/303,968
<151> 2001-07-09
<160> 166
<170> PatentIn Ver. 2.1
<210> 1
<211> 2997
<212> DNA

Cura 468 SEQ list 0705

<213> Homo sapiens

<220>

<221> misc_feature

<222> (857)..(858)

<223> wherein n is an a or t or c or g.

<220>

<221> misc_feature

<222> (2383)

<223> wherein n is an a or t or c or g.

<220>

<221> misc_feature

<222> (2983)

<223> wherein n is an a or t or c or g.

<400> 1

cgctcctgga	tgaagccccg	cgcgcgcgga	tggcggggct	tggcggcgct	gtggatgctg	60
ttggcgcagg	tggccgagca	ggtgagtccc	gggcgctccc	accagcgcgg	aaaccgcggg	120
tccggacagc	tggaggcgag	tccccgcgg	ctcctctccc	gcggaccccc	ccgtctcacc	180
gcgatgtcgc	cgctgttttc	cgcaggcacc	tgcgtgcgcc	atgggacccg	cagcggcagc	240
gcctgggagc	ccgagcgtcc	cgcgtcctcc	tccacccgcg	gagcggccgg	gctggatgga	300
aaagggcggg	acatggatga	agctggaaac	catcgttctc	agcaaactaa	cacaggaaca	360
gaaaaccaa	cactgcatgt	tctcactcaa	tatgacctgg	tctctgccta	cgaggttgac	420
cacaggggcg	attacgtgtc	ccatgaaatc	atgcaccatc	agcggcggag	aagagcagtg	480
gccgtgtccg	aggttgagtc	tcttcacctt	cggctgaaag	gccccaggca	cgacttccac	540
atggatctga	ggacttccag	cagcctagt	gctcctggct	ttattgtgca	gacgttgga	600
aagacaggca	ctaagtctgt	gcagacttta	ccgccagagg	acttctgttt	ctatcaaggc	660
tctttgcat	cacacagaaa	ctcgccatcg	catggaggga	agttctgtga	gggctccact	720
cgcactctga	agctctgcaa	cagtcagaaa	tgtccccggg	acagtgttga	cttccgtgct	780
gctcagtgtg	ccgagcacia	cagcagacga	ttcagagggc	ggcactacaa	gtggaagcct	840
tacactcaag	tagaagnnga	cttatgcaaa	ctctactgta	tcgcagaagg	atttgatttc	900
ttcttttctt	tgtcaaataa	agtcaaagat	gggactccat	gctcggagga	tagccgtaat	960
gtttgtatag	atgggatatg	tgagctcagt	gtggtgtcca	catctgcgca	catgccccag	1020
cctcccaagg	aagacctctt	catcttgcca	gatgagtata	agtcttgctt	acggcataag	1080
cgctctcttc	tgaggtccca	tagaaatgaa	gaactgaacg	tggagacctt	ggtggtggtc	1140
gacaaaaaga	tgatgcaaaa	ccatggccat	gaaaatatca	ccacctacgt	gctcacgata	1200
ctcaacatgg	tatctgcttt	attcaaagat	ggaacaatag	gaggaaacat	caacattgca	1260
attgtaggtc	tgattcttct	agaagatgaa	cagccaggac	tggtgataag	tcaccacgca	1320
gaccacacct	taagtagctt	ctgccagtgg	cagtctggat	tgatggggaa	agatgggact	1380
cgtcatgacc	acgccatctt	actgactggt	ctggatatat	gttcctggaa	gaatgagccc	1440
tgtgacactt	tgggattttg	acccataagt	ggaatgtgta	gtaaatatcg	cagctgcacg	1500
attaatgaag	atacaggtct	tggactggcc	ttcaccattg	cccatgagtc	tggacacaa	1560
tttggcata	ttcatgatgg	agaagggaac	atgtgtaaaa	agtccgaggg	caacatcatg	1620
tcccctacat	tggcaggacg	caatggagtc	ttctcctggg	caccctgcag	ccgccagtat	1680
ctacacaaat	ttctaagcac	cgctcaagct	atctgccttg	ctgatcagcc	aaagcctgtg	1740
aaggaataca	agtatcctga	gaaattgcca	ggagaattat	atgatgcaaa	cacacagtgc	1800
aagtggcagt	tcggagagaa	agccaagctc	tgcattgctg	actttaaaaa	ggacatctgt	1860
aaagccctgt	ggtgccatcg	tattggaagg	aaatgtgaga	ctaaatttat	gccagcagca	1920
gaaggcacia	tttgtgggca	tgacatgtgg	tgccggggag	gacagtgtgt	gaaatatggt	1980
gatgaaggcc	ccaagcccac	ccatggccac	tggctcgact	ggtcttcttg	gtccccatgc	2040
tccaggacct	gcggaggggg	agtatctcat	aggagtgcgc	tctgcaccaa	ccccaatcca	2100
tcgcatggag	ggaagtctct	tgagggtctc	actcgcactc	tgaagctctg	caacagtcag	2160
aaatgtcccc	gggacagtgt	tgacttccgt	gctgctcagt	gtgccgagca	caacagcaga	2220
cgattcagag	ggcggcacta	caagtggaag	cctcaggact	tatgcaaact	ctactgtatc	2280
gcagaaggat	ttgatttctt	cttttctttg	tcaaataaag	tcaaagatgg	gactccatgc	2340
tcggaggata	gccgtaattg	ttgtatagat	gggatatgtg	agnttgatg	tgacaatgtc	2400
cttggaatctg	atgctgttga	agacgtctgt	ggggtgtgta	acgggaataa	ctcagcctgc	2460
acgattcaca	ggggtctcta	caccaagcac	caccacacca	accattatca	catggtcacc	2520
attccttctg	gagcccggag	tatccgcac	tatgaaatga	acgtctctac	ctcctacatt	2580
tctgtgcgca	atgccctcag	aagggtactac	ctgaatgggc	actggaccgt	ggactggccc	2640
ggccggtaca	aattttcggg	cactactttc	gactacagac	ggtcctataa	tgagccccgag	2700

Cura 468 SEQ list 0705

aacttaatcg ctactggacc aaccaacgag acactgattg tggagctgct gtttcagggga 2760
aggaacccgg gtgttgccctg ggaatactcc atgcctcgt tggggaccga gaagcagccc 2820
cctgcccagc ccagctacac ttggggccatc gtgcgctctg agtgctccgt gtcctgcgga 2880
gggggtaggt gccttccagt gctgctcctg gaggcagcat gtcagccttc agccactgcg 2940
tacattgcac tggcctttct tgaatcctaa tgagcagccc ggngcttctc cctgcca 2997

<210> 2
<211> 986
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (283)
<223> wherein Xaa is any amino acid.

<220>
<221> VARIANT
<222> (792)
<223> wherein Xaa is any amino acid.

<400> 2
Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
1 5 10 15
Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
20 25 30
Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
35 40 45
Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
50 55 60
Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
65 70 75 80
Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
85 90 95
Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
100 105 110
Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
115 120 125
Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
130 135 140
His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
145 150 155 160
Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
165 170 175
His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
180 185 190
Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
195 200 205
Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn

Cura 468 SEQ list 0705

210						215						220				
Ser 225	Pro	Ser	His	Gly	Gly 230	Lys	Phe	Cys	Glu	Gly 235	Ser	Thr	Arg	Thr	Leu 240	
Lys	Leu	Cys	Asn	Ser 245	Gln	Lys	Cys	Pro	Arg 250	Asp	Ser	Val	Asp	Phe 255	Arg	
Ala	Ala	Gln	Cys 260	Ala	Glu	His	Asn	Ser 265	Arg	Arg	Phe	Arg	Gly 270	Arg	His	
Tyr	Lys	Trp 275	Lys	Pro	Tyr	Thr	Gln 280	Val	Glu	Xaa	Asp	Leu 285	Cys	Lys	Leu	
Tyr	Cys 290	Ile	Ala	Glu	Gly	Phe 295	Asp	Phe	Phe	Phe	Ser 300	Leu	Ser	Asn	Lys	
Val 305	Lys	Asp	Gly	Thr	Pro 310	Cys	Ser	Glu	Asp	Ser 315	Arg	Asn	Val	Cys	Ile 320	
Asp	Gly	Ile	Cys	Glu 325	Leu	Ser	Val	Val	Ser 330	Thr	Ser	Ala	His	Met 335	Pro	
Gln	Pro	Pro	Lys 340	Glu	Asp	Leu	Phe	Ile 345	Leu	Pro	Asp	Glu	Tyr 350	Lys	Ser	
Cys	Leu	Arg 355	His	Lys	Arg	Ser	Leu 360	Leu	Arg	Ser	His	Arg 365	Asn	Glu	Glu	
Leu	Asn 370	Val	Glu	Thr	Leu	Val 375	Val	Val	Asp	Lys	Lys 380	Met	Met	Gln	Asn	
His 385	Gly	His	Glu	Asn	Ile 390	Thr	Thr	Tyr	Val	Leu 395	Thr	Ile	Leu	Asn	Met 400	
Val	Ser	Ala	Leu	Phe 405	Lys	Asp	Gly	Thr	Ile 410	Gly	Gly	Asn	Ile	Asn 415	Ile	
Ala	Ile	Val	Gly 420	Leu	Ile	Leu	Leu	Glu 425	Asp	Glu	Gln	Pro	Gly 430	Leu	Val	
Ile	Ser	His 435	His	Ala	Asp	His	Thr 440	Leu	Ser	Ser	Phe	Cys 445	Gln	Trp	Gln	
Ser	Gly 450	Leu	Met	Gly	Lys	Asp 455	Gly	Thr	Arg	His	Asp 460	His	Ala	Ile	Leu	
Leu 465	Thr	Gly	Leu	Asp	Ile 470	Cys	Ser	Trp	Lys	Asn 475	Glu	Pro	Cys	Asp	Thr 480	
Leu	Gly	Phe	Ala	Pro 485	Ile	Ser	Gly	Met	Cys 490	Ser	Lys	Tyr	Arg	Ser 495	Cys	
Thr	Ile	Asn	Glu 500	Asp	Thr	Gly	Leu	Gly 505	Leu	Ala	Phe	Thr	Ile 510	Ala	His	
Glu	Ser	Gly 515	His	Asn	Phe	Gly	Met 520	Ile	His	Asp	Gly	Glu 525	Gly	Asn	Met	
Cys	Lys 530	Lys	Ser	Glu	Gly	Asn 535	Ile	Met	Ser	Pro	Thr 540	Leu	Ala	Gly	Arg	
Asn	Gly	Val	Phe	Ser	Trp	Ser	Pro	Cys	Ser	Arg	Gln	Tyr	Leu	His	Lys	

Cura 468 SEQ list 0705

545					550											560
Phe	Leu	Ser	Thr	Ala 565	Gln	Ala	Ile	Cys	Leu 570	Ala	Asp	Gln	Pro	Lys 575	Pro	
Val	Lys	Glu	Tyr 580	Lys	Tyr	Pro	Glu	Lys 585	Leu	Pro	Gly	Glu	Leu 590	Tyr	Asp	
Ala	Asn	Thr 595	Gln	Cys	Lys	Trp	Gln 600	Phe	Gly	Glu	Lys	Ala 605	Lys	Leu	Cys	
Met	Leu 610	Asp	Phe	Lys	Lys	Asp 615	Ile	Cys	Lys	Ala	Leu 620	Trp	Cys	His	Arg	
Ile 625	Gly	Arg	Lys	Cys	Glu 630	Thr	Lys	Phe	Met	Pro 635	Ala	Ala	Glu	Gly	Thr 640	
Ile	Cys	Gly	His	Asp 645	Met	Trp	Cys	Arg	Gly 650	Gly	Gln	Cys	Val	Lys 655	Tyr	
Gly	Asp	Glu	Gly 660	Pro	Lys	Pro	Thr	His 665	Gly	His	Trp	Ser	Asp 670	Trp	Ser	
Ser	Trp	Ser 675	Pro	Cys	Ser	Arg	Thr 680	Cys	Gly	Gly	Gly	Val 685	Ser	His	Arg	
Ser	Arg 690	Leu	Cys	Thr	Asn	Pro 695	Asn	Pro	Ser	His	Gly 700	Gly	Lys	Phe	Cys	
Glu 705	Gly	Ser	Thr	Arg	Thr 710	Leu	Lys	Leu	Cys	Asn 715	Ser	Gln	Lys	Cys	Pro 720	
Arg	Asp	Ser	Val	Asp 725	Phe	Arg	Ala	Ala	Gln 730	Cys	Ala	Glu	His	Asn 735	Ser	
Arg	Arg	Phe	Arg 740	Gly	Arg	His	Tyr	Lys 745	Trp	Lys	Pro	Gln	Asp 750	Leu	Cys	
Lys	Leu	Tyr 755	Cys	Ile	Ala	Glu	Gly 760	Phe	Asp	Phe	Phe	Phe 765	Ser	Leu	Ser	
Asn	Lys 770	Val	Lys	Asp	Gly	Thr 775	Pro	Cys	Ser	Glu	Asp 780	Ser	Arg	Asn	Val	
Cys 785	Ile	Asp	Gly	Ile	Cys 790	Glu	Xaa	Gly	Cys	Asp 795	Asn	Val	Leu	Gly	Ser 800	
Asp	Ala	Val	Glu	Asp 805	Val	Cys	Gly	Val	Cys 810	Asn	Gly	Asn	Asn	Ser 815	Ala	
Cys	Thr	Ile	His 820	Arg	Gly	Leu	Tyr	Thr 825	Lys	His	His	His	Thr 830	Asn	His	
Tyr	His	Met 835	Val	Thr	Ile	Pro	Ser 840	Gly	Ala	Arg	Ser	Ile 845	Arg	Ile	Tyr	
Glu	Met 850	Asn	Val	Ser	Thr	Ser 855	Tyr	Ile	Ser	Val	Arg 860	Asn	Ala	Leu	Arg	
Arg 865	Tyr	Tyr	Leu	Asn	Gly 870	His	Trp	Thr	Val	Asp 875	Trp	Pro	Gly	Arg	Tyr 880	
Lys	Phe	Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro	

Cura 468 SEQ list 0705

885

890

895

Glu Asn Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu
 900 905 910
 Leu Leu Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met
 915 920 925
 Pro Arg Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr
 930 935 940
 Trp Ala Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg
 945 950 955 960
 Cys Leu Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr
 965 970 975
 Ala Tyr Ile Ala Leu Ala Phe Leu Glu Ser
 980 985

<210> 3
 <211> 2433
 <212> DNA
 <213> Homo sapiens

<400> 3
 gtggccccta gcccctcgga gcgctcctgg atgaagcccc gcgcgcgcgg atggcggggc 60
 ttggcggcgc tgtggatgct gctggcgagc gtggccgagc aggtgagtc cgggcgctcc 120
 caccagcgcg gaaaccgcgg gtccggacag ctggaggcga gtccccgcg gctcctctcc 180
 cgcggacccc gccgtctcac cgcgatgtcg ccgctgtttt ccgcaggcac ctgcgtgcgc 240
 catgggaccc gcagcggcag cgcctgggag cccgagcgtc ccgcgtcctc ctccacccgc 300
 ggagcggccg ggctggatgg aaaagggcgg gacatggatg aagctggaaa ccatcgttct 360
 cagcaacta acacaggaac agaaaaccaa acactgcatg ttctcactcg tgaatatgac 420
 ctggtctctg cctacgaggt tgaccacagg ggcgattacg tgtcccatga aatcatgcac 480
 catcagcggc ggagaagagc agtggccgtg tccgagggtg agtctcttca ccttcggctg 540
 aaaggcccca ggcacgactt ccacatggat ctgaggactt ccagcagcct agtggctcct 600
 ggctttattg tgcagacgtt gggaaagaca ggcactaagt ctgtgcagac tttaccgcca 660
 gaggacttct gtttctatca aggctctttg cgatcacaca gaaactcccc atcgcattga 720
 ggaagttct gtgagggtc cactcgcact ctgaagctct gcaacagtca gaaatgtccc 780
 cgggacagt ttgacttccg tgctgctcag tgtgccgagc acaacagcag acgattcaga 840
 gggcggcact acaagtggaa gccttacact caagtagaac aggacttatg caaactctac 900
 tgtatcgag aaggatttga tttcttcttt tctttgtcaa ataaagtcaa agatgggact 960
 ccatgctcgg aggatagccg taatgtttgt atagatggga tatgtgagat gccccagcct 1020
 cccaaggaag acctcttcat cttgccagat gagtataagt cttgcttacg gcataagcgc 1080
 tctcttctga ggtcccatag aatgaagaa ctgaacgtgg agaccttggg ggtggtcgac 1140
 aaaaagatga tgcaaaacca tggccatgaa aatatcacca cctacgtgct cacgatactc 1200
 aacatggtat ctgctttatt caaagatgga acaataggag gaaacatcaa cattgcaatt 1260
 gtaggtctga ttcttctaga agatgaacag gacatctgta aagccctgtg gtgccatcgt 1320
 attggaagga aatgtgagac taaatttatg ccagcagcag aaggcacaat ttgtgggcat 1380
 gacatgtggg gccggggagg acagtgtgtg aaatatgggt atgaaggccc caagcccacc 1440
 catggccact ggtcggactg gtcttcttgg tccccatgct ccaggacctg cggaggggga 1500
 gtatctcata ggagtcgcct ctgcaccaac cccaggccat cgcattggag gaagttctgt 1560
 gagggctcca ctgcactct gaagctctgc aacagtcaga aatgtccccg ggacagtgtt 1620
 gacttccgtg ctgctcagtg tgccgagcac aacagcagac gattcagagg gcggcactac 1680
 aagtggaagc ctgaggactt atgcaaaact tactgtatcg cagaaggatt tgatttcttc 1740
 ttttctttgt caaataaagt caaagatggg actccatgct cggaggatag ccgtaatgtt 1800
 tgtatagatg ggatatgtga gggatgtgac aatgtccttg gatctgatgc tgttgaagac 1860
 gtctgtgggg tgtgtaacgg gaataactca gcctgcacga ttcacagggg tctctacacc 1920
 aagcaccacc acaccaacta ttatcacatg gtcaccattc cttctggagc ccggagtatc 1980
 cgcattctatg aatgaacgt ctctacctcc tacatttctg tgcgcaatgc cctcagaagg 2040
 tactacctga atgggcactg gaccgtggac tggcccggcc ggtacaaatt ttcgggcact 2100
 actttcgact acagacgggtc ctataatgag cccgagaact taatcgctac tggaccaacc 2160

Cura 468 SEQ list 0705

```

aacgagacac tgattgtgga gctgctgttt caggggaagga acccggtgtg tgcctgggaa 2220
tactccatgc ctcgcttggg gaccgagaag cagccccctg cccagcccag ctacacttgg 2280
gccatcgtgc gctctgagtg ctccgtgtcc tgcggagggg gtaggtgcct tccagtgcctg 2340
ctcctggagg cagcatgtca gccttcagcc actgcgtaca ttgcactggc ctttcttgaa 2400
tcctaatagag cagccccggg cttctccctg cca 2433

```

<210> 4
 <211> 791
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
 1 5 10 15
 Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
 20 25 30
 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
 35 40 45
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 50 55 60
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 65 70 75 80
 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95
 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 100 105 110
 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Arg Glu
 115 120 125
 Tyr Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val
 130 135 140
 Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val
 145 150 155 160
 Ser Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp
 165 170 175
 Phe His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe
 180 185 190
 Ile Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu
 195 200 205
 Pro Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg
 210 215 220
 Asn Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr
 225 230 235 240
 Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe
 245 250 255
 Arg Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg
 260 265 270

Cura 468 SEQ list 0705

His	Tyr	Lys 275	Trp	Lys	Pro	Tyr	Thr 280	Gln	Val	Glu	Gln	Asp 285	Leu	Cys	Lys		
Leu	Tyr 290	Cys	Ile	Ala	Glu	Gly 295	Phe	Asp	Phe	Phe	Phe 300	Ser	Leu	Ser	Asn		
Lys 305	Val	Lys	Asp	Gly	Thr 310	Pro	Cys	Ser	Glu	Asp 315	Ser	Arg	Asn	Val	Cys 320		
Ile	Asp	Gly	Ile	Cys 325	Glu	Met	Pro	Gln	Pro 330	Pro	Lys	Glu	Asp	Leu 335	Phe		
Ile	Leu	Pro	Asp 340	Glu	Tyr	Lys	Ser	Cys 345	Leu	Arg	His	Lys	Arg 350	Ser	Leu		
Leu	Arg	Ser 355	His	Arg	Asn	Glu	Glu 360	Leu	Asn	Val	Glu	Thr 365	Leu	Val	Val		
Val	Asp 370	Lys	Lys	Met	Met	Gln 375	Asn	His	Gly	His	Glu 380	Asn	Ile	Thr	Thr		
Tyr 385	Val	Leu	Thr	Ile	Leu 390	Asn	Met	Val	Ser	Ala 395	Leu	Phe	Lys	Asp	Gly 400		
Thr	Ile	Gly	Gly	Asn 405	Ile	Asn	Ile	Ala	Ile 410	Val	Gly	Leu	Ile	Leu 415	Leu		
Glu	Asp	Glu	Gln 420	Asp	Ile	Cys	Lys	Ala 425	Leu	Trp	Cys	His	Arg 430	Ile	Gly		
Arg	Lys	Cys 435	Glu	Thr	Lys	Phe	Met 440	Pro	Ala	Ala	Glu	Gly 445	Thr	Ile	Cys		
Gly	His 450	Asp	Met	Trp	Cys	Arg 455	Gly	Gly	Gln	Cys	Val 460	Lys	Tyr	Gly	Asp		
Glu 465	Gly	Pro	Lys	Pro	Thr 470	His	Gly	His	Trp	Ser 475	Asp	Trp	Ser	Ser	Trp 480		
Ser	Pro	Cys	Ser	Arg 485	Thr	Cys	Gly	Gly	Gly 490	Val	Ser	His	Arg	Ser 495	Arg		
Leu	Cys	Thr	Asn 500	Pro	Arg	Pro	Ser	His 505	Gly	Gly	Lys	Phe	Cys 510	Glu	Gly		
Ser	Thr	Arg 515	Thr	Leu	Lys	Leu	Cys 520	Asn	Ser	Gln	Lys	Cys 525	Pro	Arg	Asp		
Ser	Val 530	Asp	Phe	Arg	Ala	Ala 535	Gln	Cys	Ala	Glu	His 540	Asn	Ser	Arg	Arg		
Phe 545	Arg	Gly	Arg	His	Tyr 550	Lys	Trp	Lys	Pro	Gln 555	Asp	Leu	Cys	Lys	Leu 560		
Tyr	Cys	Ile	Ala	Glu 565	Gly	Phe	Asp	Phe	Phe 570	Phe	Ser	Leu	Ser	Asn 575	Lys		
Val	Lys	Asp	Gly 580	Thr	Pro	Cys	Ser	Glu 585	Asp	Ser	Arg	Asn	Val 590	Cys	Ile		
Asp	Gly	Ile 595	Cys	Glu	Gly	Cys	Asp 600	Asn	Val	Leu	Gly	Ser 605	Asp	Ala	Val		

Cura 468 SEQ list 0705

Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
610 615 620

His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Tyr Tyr His Met
625 630 635 640

Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn
645 650 655

Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr
660 665 670

Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser
675 680 685

Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu
690 695 700

Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe
705 710 715 720

Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu
725 730 735

Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile
740 745 750

Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu Pro
755 760 765

Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr Ile
770 775 780

Ala Leu Ala Phe Leu Glu Ser
785 790

<210> 5
<211> 2902
<212> DNA
<213> Homo sapiens

<400> 5

ttggcggcgc	tgtggatgct	gctggcgcag	gtggccgagc	aggtgagtcc	cgggcgctcc	60
caccagcgcg	gaaaccgcgg	gtccggacag	ctggaggcga	gtcccccgcg	gctcctctcc	120
cgcggacccc	gccgtctcac	cgcgatgtcg	ccgctgtttt	ccgcaggcac	ctgcgtgcgc	180
catgggaccc	gcagcggcag	cgcctgggag	cccagcgtc	ccgcgtcctc	ctccagacct	240
ggtctctgcc	tacgaggttg	accacagggg	cgattacgtg	tcccatgaaa	tcatgcacca	300
tcagcggcgg	agaagagcag	tggccgtgtc	cgaggttgag	ccagcctttc	tccaggtatg	360
cagagccaga	gagctcagac	tgtgtgtgga	ggcctttccc	attgctaatt	ctcagccggg	420
gtttttgaac	ctttccaatg	ttcgctctca	ctggagggaa	cagcatgctt	ccaagagaat	480
aataacaaat	gcaatgcttg	gagaatcggc	cctggcttca	accagaaagt	ctaatttgtg	540
tttctttctt	tccttttatt	ttttccagtc	aggcatgata	cgaacagaag	aggcagatta	600
cttcctaagg	ccacttcctt	cacacctctc	atggaaactc	ggcagagctg	ccaaggcag	660
ctcgccatcc	cacgtactgt	acaagagaga	ggtcctggtg	acctcaagga	catgggagct	720
ggcacatcaa	cccctgcaca	gcagcgacct	tcgcctggga	ctgccacaaa	agcagcattt	780
ctgtggaaga	cgcaagaaat	acatgcccc	gcctcccaag	gaagacctct	tcatcttgcc	840
agatgagtat	aagtcttgct	tacggcataa	gcgctctctt	ctgaggtccc	atagaaatga	900
agaactgaac	gtggagacct	tggttggtgg	cgacaaaaag	atgatgcaaa	accatggcca	960
tgaatatatc	accacctacg	tgctcacgat	actcaacatg	gtatctgctt	tattcaaaga	1020
tggaacaata	ggaggaaaca	tcaacattgc	aattgtaggt	ctgattcttc	tagaagatga	1080
acagccagga	ctggtgataa	gtcaccacgc	agaccacacc	ttaagtagtt	tctgccagtg	1140

Cura 468 SEQ list 0705

```

gcagtctgga ttgatgggga aagatgggac tcgtcatgac cacgccatct tactgactgg 1200
tctggatata tgttcctgga agaattgagcc ctgtgacact ttgggatttg cacccataag 1260
tggaatgtgt agtaaatatc gcagctgcac gattaatgaa gatacaggtc ttggactggc 1320
cttcaccatt gcccatgagt ctggacacaa ctttggcatg attcatgatg gagaagggaa 1380
catgtgcaaa aagtccgagg gcaacatcat gtcccctaca ttggcaggac gcaatggagt 1440
cttctcctgg tcaccctgca gccgccagta tctacacaaa tttctaagca ccgctcaagc 1500
tatctgcctt gctgatcagc caaagcctgt gaaggaatac aagtatcctg agaaattgcc 1560
aggagaatta tatggtgcaa acacacagtg caagtggcag ttcggagaga aagccaagct 1620
ctgcatgctg gacttttaaa aggacatctg taaagccctg tgggtgccatc gtattggaag 1680
gaaatgtgag actaaattta tgccagcagc agaaggcaca atttgtgggc atgaacatgg 1740
tgccggagga cagtgtgtga aatatgggtga tgaaggcccc aagcccaccc atggccactg 1800
gtcggactgg tcttcttggg ccccatgctc caggacctgc ggagggggag tatctcatag 1860
gagtcgctct caaaatacac attccaggcc atcgcatgga ggggaagttct gtgagggctc 1920
cactcgcact ctgaagctct gcaacagtca gaaatgtccc cgggacagtg ttgacttccg 1980
tgctgctcag tgtgccgagc acaacagcag acgattcaga gggcggcact acaagtggaa 2040
gcctgatcag gacttatgca aactctactg tatcgagaa ggatttgatt tcttcttttc 2100
tttgtcaaat aaagtcaaag atgggactcc atgctcggag gatagccgta atgtttgtat 2160
agatgggata tgtgagagag ttggatgtga caatgtcctt ggatctgatg ctgttgaaga 2220
cgtctgtggg gtgtgtaacg ggaataactc agcctgcacg attcacaggg gtctctacct 2280
agagtattat cacatggtca ccattccttc tggagcccg agtatccgca tctatgaaat 2340
gaacgtctct acctcctaca tttctgtgcg caatgccctc agaagggtact acctgaatgg 2400
gcactggacc gtggactggc ccggccggta caaattttcg ggcactactt tcgactacag 2460
acggtcctat aatgagcccc agaacttaat cgctactgga ccaaccaacg agacactgat 2520
tgtggagctg ctgtttcagg gaaggaaccc ggggtgttgcc tgggaatact ccatgcctcg 2580
cttggggacc gagaagcagc cccctgcccc gccagctac acttggggca tcgtgcgctc 2640
tgagtgtccc gtgtcctgcg gagggggtag gtgccttcca gtgctgctcc tggaggcagc 2700
atgtcagcct ttagccactg cgtacattgc actggccttt cttgaatcct aatgagcagc 2760
ccgggggcttc tccctgccag tagcagtgc attcccaagg tggggagtgg tggctcctgag 2820
tgtcacttgt cggtcccgagc tgccttctcc agtctatctg cttcagtgtg tgactctgag 2880
gaagtcagta gatgcattgc tt                                     2902

```

<210> 6
 <211> 856
 <212> PRT
 <213> Homo sapiens

<400> 6

```

Met Gly Pro Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro
 1           5           10           15
Pro Pro Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr
           20           25           30
Val Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala
           35           40           45
Val Ser Glu Val Glu Pro Ala Phe Leu Gln Val Cys Arg Ala Arg Glu
           50           55           60
Leu Arg Leu Cys Val Glu Ala Phe Pro Ile Ala Asn Ser Gln Pro Gly
           65           70           75           80
Phe Leu Asn Leu Ser Asn Val Arg Ser His Trp Arg Glu Gln His Ala
           85           90           95
Ser Lys Arg Ile Ile Thr Asn Ala Met Leu Gly Glu Ser Ala Leu Ala
           100          105          110
Ser Thr Arg Lys Ser Asn Cys Val Phe Phe Leu Ser Phe Tyr Phe Phe
           115          120          125
Gln Ser Gly Met Ile Arg Thr Glu Glu Ala Asp Tyr Phe Leu Arg Pro

```

Cura 468 SEQ list 0705

130		135		140
Leu 145	Pro	Ser	His	Leu 150
Ser	Pro	Ser	His	Val 165
Thr	Trp	Glu	Leu 180	Ala
Gly	Leu	Pro 195	Gln	Lys
Pro	Gln	Pro	Pro	Lys
Ser	Cys	Leu	Arg	His
Glu	Leu	Asn	Val	Glu
Asn	His	Gly	His	Glu
Met	Val	Ser	Ala	Leu
Ile	Ala	Ile	Val	Gly
Val	Ile	Ser	His	His
Gln	Ser	Gly	Leu	Met
Leu	Leu	Thr	Gly	Leu
Thr	Leu	Gly	Phe	Ala
Cys	Thr	Ile	Asn	Glu
His	Glu	Ser	Gly	His
Met	Cys	Lys	Lys	Ser
Arg	Asn	Gly	Val	Phe
Lys	Phe	Leu	Ser	Thr
Pro	Val	Lys	Glu	Tyr
Gly	Ala	Asn	Thr	Gln

Cura 468 SEQ list 0705
475

465					470											480
Cys	Met	Leu	Asp	Phe 485	Lys	Lys	Asp	Ile	Cys 490	Lys	Ala	Leu	Trp	Cys 495	His	
Arg	Ile	Gly	Arg 500	Lys	Cys	Glu	Thr	Lys 505	Phe	Met	Pro	Ala	Ala 510	Glu	Gly	
Thr	Ile	Cys 515	Gly	His	Glu	His	Gly 520	Ala	Gly	Gly	Gln	Cys 525	Val	Lys	Tyr	
Gly	Asp 530	Glu	Gly	Pro	Lys	Pro 535	Thr	His	Gly	His	Trp 540	Ser	Asp	Trp	Ser	
Ser	Trp	Ser	Pro	Cys	Ser 550	Arg	Thr	Cys	Gly	Gly 555	Gly	Val	Ser	His	Arg 560	
Ser	Arg	Ser	Gln	Asn 565	Thr	His	Ser	Arg	Pro 570	Ser	His	Gly	Gly	Lys 575	Phe	
Cys	Glu	Gly	Ser 580	Thr	Arg	Thr	Leu	Lys 585	Leu	Cys	Asn	Ser	Gln 590	Lys	Cys	
Pro	Arg	Asp 595	Ser	Val	Asp	Phe	Arg 600	Ala	Ala	Gln	Cys	Ala 605	Glu	His	Asn	
Ser	Arg 610	Arg	Phe	Arg	Gly	Arg 615	His	Tyr	Lys	Trp	Lys 620	Pro	Asp	Gln	Asp	
Leu	Cys	Lys	Leu	Tyr	Cys 630	Ile	Ala	Glu	Gly	Phe 635	Asp	Phe	Phe	Phe	Ser 640	
Leu	Ser	Asn	Lys	Val 645	Lys	Asp	Gly	Thr	Pro 650	Cys	Ser	Glu	Asp	Ser 655	Arg	
Asn	Val	Cys	Ile 660	Asp	Gly	Ile	Cys	Glu 665	Arg	Val	Gly	Cys	Asp 670	Asn	Val	
Leu	Gly	Ser 675	Asp	Ala	Val	Glu	Asp 680	Val	Cys	Gly	Val	Cys 685	Asn	Gly	Asn	
Asn	Ser 690	Ala	Cys	Thr	Ile	His 695	Arg	Gly	Leu	Tyr	Leu 700	Glu	Tyr	Tyr	His	
Met	Val	Thr	Ile	Pro	Ser 710	Gly	Ala	Arg	Ser	Ile 715	Arg	Ile	Tyr	Glu	Met 720	
Asn	Val	Ser	Thr	Ser 725	Tyr	Ile	Ser	Val	Arg 730	Asn	Ala	Leu	Arg	Arg 735	Tyr	
Tyr	Leu	Asn	Gly 740	His	Trp	Thr	Val	Asp 745	Trp	Pro	Gly	Arg	Tyr 750	Lys	Phe	
Ser	Gly	Thr 755	Thr	Phe	Asp	Tyr	Arg 760	Arg	Ser	Tyr	Asn	Glu 765	Pro	Glu	Asn	
Leu	Ile 770	Ala	Thr	Gly	Pro	Thr 775	Asn	Glu	Thr	Leu	Ile 780	Val	Glu	Leu	Leu	
Phe	Gln	Gly	Arg	Asn	Pro 790	Gly	Val	Ala	Trp	Glu 795	Tyr	Ser	Met	Pro	Arg 800	
Leu	Gly	Thr	Glu	Lys	Gln	Pro	Pro	Ala	Gln	Pro	Ser	Tyr	Thr	Trp	Ala	

Cura 468 SEQ list 0705

805

810

815

Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu
 820 825 830

Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Leu Ala Thr Ala Tyr
 835 840 845

Ile Ala Leu Ala Phe Leu Glu Ser
 850 855

<210> 7

<211> 2895

<212> DNA

<213> Homo sapiens

<400> 7

cgctcctgga	tgaagccccg	cgcgcgcgga	tggcggggct	tggcggcgct	gtggatgctg	60
ttggcgcagg	tggccgagca	ggtgagtccc	gggcgctccc	accagcgcgg	aaaccgcggg	120
tccggacagc	tggaggcgag	tccccgcg	ctcctctccc	gcggaccccc	ccgtctcacc	180
gcgatgtcgc	cgctgttttc	cgcaggcacc	tgcgtgcgcc	atgggacccc	cagcggcagc	240
gcctgggagc	ccgagcgtcc	cgcgtcctcc	tccacccgcg	gagcggccgg	gctggatgga	300
aaagggcggg	acatggatga	agctggaaac	catcgttctc	agcaaactaa	cacaggaaca	360
gaaaaccaa	cactgcatgt	tctcactcaa	tatgacctgg	tctctgccta	cgagggtgac	420
cacagggg	attacgtgtc	ccatgaaatc	atgcaccatc	agcggcggag	aagagcagtg	480
gccgtgtccg	aggttgagtc	tcttcacctt	cggctgaaag	gccccaggca	cgacttccac	540
atggatctga	ggacttccag	cagcctagt	gctcctggct	ttattgtgca	gacgttgga	600
aagacaggca	ctaagtctgt	gcagacttta	ccgccagagg	acttctgttt	ctatcaaggc	660
tctttgcat	cacacagaaa	ctcgccatcg	catggaggga	agttctgtga	gggctccact	720
cgcactctga	agctctgcaa	cagtcagaaa	tgtccccggg	acagtgttga	cttccgtgct	780
gctcagtgtg	ccgagcacaa	cagcagacga	ttcagagggc	ggcactacaa	gtggaagcct	840
tacactcaag	tagaagccga	cttatgcaaa	ctctactgta	tcgcagaagg	atttgatttc	900
ttcttttctt	tgtcaaataa	agtcaaagat	gggactccat	gctcggagga	tagccgtaat	960
gtttgtatag	atgggatatg	tgagctcagt	gtggtgtcca	catctgcgca	catgccccag	1020
cctcccaagg	aagacctctt	catcttgcca	gatgagtata	agtcttgctt	acggcataag	1080
cgctctcttc	tgaggtccca	tagaaatgaa	gaactgaacg	tggagacctt	ggtggtggtc	1140
gacaaaaaga	tgatgcaaaa	ccatggccat	gaaaatatca	ccacctacgt	gctcacgata	1200
ctcaacatgg	tatctgcttt	attcaaagat	ggattgatgg	ggaaagatgg	gactcgtcat	1260
gaccacgcca	tcttactgac	tggtctggat	atatgttcct	ggaagaatga	gccctgtgac	1320
actttgggat	ttgcacccat	aagtggaaatg	tgtagtaa	atcgcagctg	cacgattaat	1380
gaagatacag	gtcttgagct	ggccttcacc	attgccccatg	agtctggaca	caactttggc	1440
atgattcatg	atggagaagg	gaacatgtgt	aaaaagtccg	agggcaacat	catgtcccct	1500
acattggcag	gacgcaatgg	agtcttctcc	tggtcaccct	gcagccgcca	gtatctacac	1560
aaattttctaa	gcaccgctca	agctatctgc	cttgctgatc	agccaaagcc	tgtgaaggaa	1620
tacaagtatc	ctgagaaaatt	gccaggagaa	ttatatgatg	caaacacaca	gtgcaagtgg	1680
cagttcggag	agaaagccaa	gctctgcatg	ctggacttta	aaaaggacat	ctgtaaagcc	1740
ctgtggtgcc	atcgtattgg	aaggaaatgt	gagactaaat	ttatgccagc	agcagaaggc	1800
acaattttgtg	ggcatgacat	gtggtgccgg	ggaggacagt	gtgtgaaata	tggtgatgaa	1860
ggccccaagc	ccacccatgg	ccactggtcg	gactggctct	cttggtcccc	atgctccagg	1920
acctgcggag	ggggagtatc	tcataggagt	cgcctctgca	ccaaccccaa	gccatcgc	1980
ggaggggaagt	tctgtgaggg	ctccactcgc	actctgaagc	tctgcaacag	tcagaaatgt	2040
ccccgggaca	gtgttgactt	ccgtgctgct	cagtgtgccg	agcacaacag	cagacgattc	2100
agagggcggc	actacaagt	gaagccttac	actcaagtag	aagatcagga	cttatgcaaa	2160
ctctactgta	tcgcagaagg	atttgatttc	ttcttttctt	tgtcaaataa	agtcaaagat	2220
gggactccat	gctcggagga	tagccgtaat	gtttgtatag	atgggatatg	tgagagagtt	2280
ggatgtgaca	atgtccttgg	atctgatgct	gttgaagacg	tctgtgggg	gtgtaacggg	2340
aataactcag	cctgcacgat	tcacaggggt	ctctacacca	agcaccacca	caccaaccag	2400
tattatcaca	tggtcaccat	tccttctgga	gcccggagta	tccgcatcta	tgaaatgaac	2460
gtctctac	cctacatttc	tgtgcgcaat	gccctcagaa	ggtactacct	gaatgggcac	2520
tggaccgtgg	actggccccg	ccggtacaaa	ttttcgggca	ctactttcga	ctacagacgg	2580
tcctataatg	agcccagagaa	cttaatcgct	actggaccaa	ccaacgagac	actgattgtg	2640
gagctgctgt	ttcaggggaag	gaacccgggt	gttgcctggg	aatactccat	gcctcgcctg	2700

Cura 468 SEQ list 0705

gggaccgaga agcagccccc tgcccagccc agctacactt gggccatcgt gcgctctgag 2760
 tgctccgtgt cctgcggagg gggtaggtgc cttccagtgc tgctcctgga ggcagcatgt 2820
 cagccttcag ccactgcgta cattgcactg gcctttcttg aatcctaata agcagcccgg 2880
 ggcttctccc tgcca 2895

<210> 8
 <211> 952
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
 1 5 10 15
 Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
 20 25 30
 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
 35 40 45
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 50 55 60
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 65 70 75 80
 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95
 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 100 105 110
 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
 115 120 125
 Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
 130 135 140
 His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
 145 150 155 160
 Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
 165 170 175
 His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
 180 185 190
 Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
 195 200 205
 Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn
 210 215 220
 Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu
 225 230 235 240
 Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg
 245 250 255
 Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His
 260 265 270

Cura 468 SEQ list 0705

Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Ala	Asp	Leu	Cys	Lys	Leu
		275					280					285			
Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys
	290					295					300				
Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile
305					310					315					320
Asp	Gly	Ile	Cys	Glu	Leu	Ser	Val	Val	Ser	Thr	Ser	Ala	His	Met	Pro
				325					330					335	
Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys	Ser
			340					345					350		
Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	Glu
		355					360					365			
Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln	Asn
	370					375					380				
His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn	Met
385					390					395					400
Val	Ser	Ala	Leu	Phe	Lys	Asp	Gly	Leu	Met	Gly	Lys	Asp	Gly	Thr	Arg
				405					410					415	
His	Asp	His	Ala	Ile	Leu	Leu	Thr	Gly	Leu	Asp	Ile	Cys	Ser	Trp	Lys
			420					425					430		
Asn	Glu	Pro	Cys	Asp	Thr	Leu	Gly	Phe	Ala	Pro	Ile	Ser	Gly	Met	Cys
		435					440					445			
Ser	Lys	Tyr	Arg	Ser	Cys	Thr	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Gly	Leu
	450					455					460				
Ala	Phe	Thr	Ile	Ala	His	Glu	Ser	Gly	His	Asn	Phe	Gly	Met	Ile	His
465					470					475					480
Asp	Gly	Glu	Gly	Asn	Met	Cys	Lys	Lys	Ser	Glu	Gly	Asn	Ile	Met	Ser
				485					490					495	
Pro	Thr	Leu	Ala	Gly	Arg	Asn	Gly	Val	Phe	Ser	Trp	Ser	Pro	Cys	Ser
			500					505					510		
Arg	Gln	Tyr	Leu	His	Lys	Phe	Leu	Ser	Thr	Ala	Gln	Ala	Ile	Cys	Leu
		515					520					525			
Ala	Asp	Gln	Pro	Lys	Pro	Val	Lys	Glu	Tyr	Lys	Tyr	Pro	Glu	Lys	Leu
	530					535					540				
Pro	Gly	Glu	Leu	Tyr	Asp	Ala	Asn	Thr	Gln	Cys	Lys	Trp	Gln	Phe	Gly
545					550					555					560
Glu	Lys	Ala	Lys	Leu	Cys	Met	Leu	Asp	Phe	Lys	Lys	Asp	Ile	Cys	Lys
				565					570					575	
Ala	Leu	Trp	Cys	His	Arg	Ile	Gly	Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met
			580					585					590		
Pro	Ala	Ala	Glu	Gly	Thr	Ile	Cys	Gly	His	Asp	Met	Trp	Cys	Arg	Gly
		595					600					605			

Cura 468 SEQ list 0705

Gly Gln Cys Val Lys Tyr Gly Asp Glu Gly Pro Lys Pro Thr His Gly
610 615 620

His Trp Ser Asp Trp Ser Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly
625 630 635 640

Gly Gly Val Ser His Arg Ser Arg Leu Cys Thr Asn Pro Lys Pro Ser
645 650 655

His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys
660 665 670

Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln
675 680 685

Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp
690 695 700

Lys Pro Tyr Thr Gln Val Glu Asp Gln Asp Leu Cys Lys Leu Tyr Cys
705 710 715 720

Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys Val Lys
725 730 735

Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile Asp Gly
740 745 750

Ile Cys Glu Arg Val Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val
755 760 765

Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
770 775 780

His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Gln Tyr Tyr His
785 790 795 800

Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met
805 810 815

Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr
820 825 830

Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe
835 840 845

Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn
850 855 860

Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu
865 870 875 880

Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg
885 890 895

Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala
900 905 910

Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu
915 920 925

Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr
930 935 940

Ile Ala Leu Ala Phe Leu Glu Ser
945 950

<210> 9
<211> 4488
<212> DNA
<213> Homo sapiens

<400> 9
atgtgggctc agctccttct aggaatgttg gccctatcac cagccattgc agaagaactt 60
ccaaactacc tgggtgacatt accagcccgg ctaaatttcc cctccgttca gaaggtttgt 120
ttggacctga gccctgggta cagtgatgtt aaattcacgg ttactctgga gaccaaggac 180
aagaccaga agttgctaga atactctgga ctgaagaaga ggcacttaca ttgtatctcc 240
tttcttgtag cacctcctgc tgggtggcaca gaagaagtgg ccacaatccg ggtgtcggga 300
gttggaata acatcagctt tgaggagaag aaaaagggtc taattcagag gcaggggaac 360
ggcacctttg tacagactga caaacctctc tacaccccag ggcagcaagt gtatttccgc 420
attgtcacca tggatagcaa cttcgttcca gtgaatgaca agtactccat ggtggaacta 480
caggatccaa atagcaacag gattgcacag tggctggaag tggtagctga gcaaggcatt 540
gtagacctgt ccttccaact ggcaccagag gcaatgctgg gcacctacac tgtggcagtg 600
gctgagggca agacctttgg tactttcagt gtggaggaat atgtgctttc tccatttctc 660
cttttactct cttcagtgtc gccgaagtgt aagggtggaag tgggtggaacc caaggagtta 720
tcaacggtgc aggaatcttt cttagtaaaa atttgttgta ggtacaccta tggaaagccc 780
atgctagggg cagtgcaggt atctgtgtgt cagaaggcaa atacttactg gtatcgagag 840
gtggaacggg aacagcttcc tgacaaatgc aggaacctct ctggacagac tgacaaaaca 900
ggatgtttct cagcacctgt ggacatggcc acctttgacc tcattggata tgcgtacagc 960
catcaaata atattgtggc tactgttgtg gaggaaggga cagggtgtga ggccaatgcc 1020
actcagaata tctacatttc tccacaaatg ggatcaatga cctttgaaga caccagcaat 1080
ttttaccatc caaatttccc cttcagtggg aagatgctgc tcaagtttcc gcaaggcggc 1140
gtgctccctt gcaagaacca tctagtgttt ctggtgattt atggcacaaa tggaaacctt 1200
aaccagacct tggttactga taacaatggc ctagctccct ttaccttga gacatccggc 1260
tggaatggga cagacgtttc tctggaggga aagtttcaaa tggaaagactt agtatataat 1320
ccggaacaag tgccacgtta ctaccaaata gcctacctgc acctgcgacc cttctacagc 1380
acaaccgca gcttccttgg catccaccgg ctaaacggcc ccttgaaatg tggccagccc 1440
caggaagtgc tgggtgatta ttacatcgac ccggccgatg caagccctga ccaagagatc 1500
agcttctcct actatttaat agggaaagga agtttgggtg tggaggggca gaaacacctg 1560
aactctaaga agaaaggact gaaagcctcc ttctctctct cactgacctt cacttcgaga 1620
ctggcccctg atccttccct ggtgatctat gccatttttc ccagtggagg tgttgtagct 1680
gacaaaattc agttctcagt cgagatgtgc tttgacaatc agcagcttcc aggagcagaa 1740
gtggagctgc agctgcaggc agctcccgga tccctgtgtg cgctccgggc ggtggatgag 1800
agtgtcttac tgcttaggcc agacagagag ctgagcaacc gctctgtcta tgggatgttt 1860
ccattctggt atggtcacta cccctatcaa gtggctgagt atgatcagtg tccagtgtct 1920
ggcccatggg actttcctca gccctcatt gacccaatgc cccaagggca ttcgagccag 1980
cgttccatta tctggaggcc ctcgttctct gaaggcacgg accttttcag ctttttccgg 2040
gacgtgggcc tgaaaatact gtccaatgcc aaaatcaaga agccagtaga ttgcagtcac 2100
agatctccag aatacagcac tgctatgggt ggcgggtggc atccagaggc ttttgagtca 2160
tcaactcctt tacatcaagc agaggattct caggtccgcc agtacttccc agagacctgg 2220
ctctgggatc tgtttcctat tggtaactcg ggggaaggag cgggtccacgt cacagttcct 2280
gacgccatca ccgagtggaa ggcgatgagt ttctgcactt cccagtcaag aggcttcggg 2340
ctttcaccca ctgttggaact aactgctttc aagccgttct ttgttgacct gactctccct 2400
tactcagtag tccgtgggga atcctttcgt cttactgcca ccatcttcaa ttacctaaag 2460
gattgcatca gggttcagac tgacctggct aaatcgcatg agtaccagct agaatacatg 2520
gcagattctc agacctccag ttgtctctgt gctgatgacg caaaaaccca ccactggaac 2580
atcacagctg tcaaattggg tcacattaac ttactatta gtacaaagat tctggacagc 2640
aatgaaccat gtggggggcca gaagggtgtt gttcccaaaa agggccgaag tgacacgctc 2700
atcaagccag ttctcgtcaa acctgaggga gtcctgggtg agaagacaca cagctcattg 2760
ctgtgcccaa aaggaggaaa ggtggcatct gaatctgtct ccctggagct cccagtggac 2820
attgttcctg actcgaccaa ggcttatgtt acggttcttg gagacattat gggcacagcc 2880
ctgcagaacc tggatggtct ggtgcagatg cccagtggct gtggcgagca gaacatggc 2940
ttgtttgctc ccatcatcta tgtcttgtag tacctggaga aggcagggct gctgacggag 3000
gagatcaggt ctcggggcagt gggtttcctg gaaatagggt accagaagga gctgatgtac 3060
aaacacagca atgggtcata cagtgccttt ggggagcgag atggaaatgg aaacacatgg 3120
ctgacagcgt ttgtcacaaa atgctttggc caagctcaga aattcatctt cattgatccc 3180

Cura 468 SEQ list 0705

```

aagaacatcc aggatgctct caagtggatg gcaggaaacc agctccccag tggctgctat 3240
gccaacgtgg gaaatctcct tcacacagct atgaagggtg gtgttgatga tgaggtctcc 3300
ttgactgctg atgtcacagc tgcattgctg gagatgggaa aggatgtaga tgaccaatg 3360
gtgagtcagg gtctacggtg tctcaagaat tcggccacct ccacgaccaa cctctacaca 3420
caggccctgt tggcttacat tttctccctg gctggggaaa tggacatcag aaacattctc 3480
cttaaacagt tagatcaaca ggctatcatc tcaggagaat ccatttactg gagccagaaa 3540
cctactccat catcgaacgc cagcccttgg tctgagcctg cggctgtaga tgtggaactc 3600
acagcatatg cattgttggc ccagcttacc aagcccagcc tgactcaaaa ggagatagcg 3660
aaggccacta gcatagtggc ttggttggcc aagcaacaca atgcatatgg gggcttctct 3720
tctactcagg atactgtagt tgctctccaa gctcttgcca aatatgccac taccgcctac 3780
atgccatctg aggagatcaa cctggttgta aaatccactg agaatttcca gcgcacattc 3840
aacatacagt cagttaacag attggtattt cagcaggata ccctgcccac tgtccctgga 3900
atgtacacgt tggaggcctc aggccagggc tgtgtctatg tgcagacggt gttgagatac 3960
aatattctcc ctcccacaaa tatgaagacc tttagtctta gtgtggaaat aggaaaagct 4020
agatgtgagc aaccgacttc acctcgatcc ttgactctca ctattcacac cagttatgtg 4080
gggagccgta gctcttccaa tatggctatt gtggaagtga agatgctatc tgggttcagt 4140
cccatggagg gcaccaatca gttacttctc cagcaacccc tgggtgaagaa ggttgaattt 4200
ggaactgaca cacttaacat ttacttggat gagctcatta agaacactca gacttacacc 4260
ttcaccatca gccaaagtgt gctggtcacc aacttgaaac cagcaaccat caaggtctat 4320
gactactacc taccaggttc ttttaaatta tctcagtaca caattgtgtg gtccatgaac 4380
aatgacagca tagtggactc tgtggcacgg caccagaaac caccctttt caagacagaa 4440
gcatttatcc cttcacttcc tgggagtgtt aacaactgat agctacca 4488

```

<210> 10

<211> 1492

<212> PRT

<213> Homo sapiens

<400> 10

```

Met Trp Ala Gln Leu Leu Leu Gly Met Leu Ala Leu Ser Pro Ala Ile
  1              5              10              15

Ala Glu Glu Leu Pro Asn Tyr Leu Val Thr Leu Pro Ala Arg Leu Asn
      20              25              30

Phe Pro Ser Val Gln Lys Val Cys Leu Asp Leu Ser Pro Gly Tyr Ser
      35              40              45

Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
      50              55              60

Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
      65              70              75              80

Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
      85              90              95

Arg Val Ser Gly Val Gly Asn Asn Ile Ser Phe Glu Glu Lys Lys Lys
      100             105             110

Val Leu Ile Gln Arg Gln Gly Asn Gly Thr Phe Val Gln Thr Asp Lys
      115             120             125

Pro Leu Tyr Thr Pro Gly Gln Gln Val Tyr Phe Arg Ile Val Thr Met
      130             135             140

Asp Ser Asn Phe Val Pro Val Asn Asp Lys Tyr Ser Met Val Glu Leu
      145             150             155             160

Gln Asp Pro Asn Ser Asn Arg Ile Ala Gln Trp Leu Glu Val Val Pro
      165             170             175

```

Cura 468 SEQ list 0705

Glu Gln Gly Ile Val Asp Leu Ser Phe Gln Leu Ala Pro Glu Ala Met
 180 185 190
 Leu Gly Thr Tyr Thr Val Ala Val Ala Glu Gly Lys Thr Phe Gly Thr
 195 200 205
 Phe Ser Val Glu Glu Tyr Val Leu Ser Pro Phe Leu Leu Leu Ser
 210 215 220
 Ser Val Leu Pro Lys Phe Lys Val Glu Val Val Glu Pro Lys Glu Leu
 225 230 235 240
 Ser Thr Val Gln Glu Ser Phe Leu Val Lys Ile Cys Cys Arg Tyr Thr
 245 250 255
 Tyr Gly Lys Pro Met Leu Gly Ala Val Gln Val Ser Val Cys Gln Lys
 260 265 270
 Ala Asn Thr Tyr Trp Tyr Arg Glu Val Glu Arg Glu Gln Leu Pro Asp
 275 280 285
 Lys Cys Arg Asn Leu Ser Gly Gln Thr Asp Lys Thr Gly Cys Phe Ser
 290 295 300
 Ala Pro Val Asp Met Ala Thr Phe Asp Leu Ile Gly Tyr Ala Tyr Ser
 305 310 315 320
 His Gln Ile Asn Ile Val Ala Thr Val Val Glu Glu Gly Thr Gly Val
 325 330 335
 Glu Ala Asn Ala Thr Gln Asn Ile Tyr Ile Ser Pro Gln Met Gly Ser
 340 345 350
 Met Thr Phe Glu Asp Thr Ser Asn Phe Tyr His Pro Asn Phe Pro Phe
 355 360 365
 Ser Gly Lys Met Leu Leu Lys Phe Pro Gln Gly Gly Val Leu Pro Cys
 370 375 380
 Lys Asn His Leu Val Phe Leu Val Ile Tyr Gly Thr Asn Gly Thr Phe
 385 390 395 400
 Asn Gln Thr Leu Val Thr Asp Asn Asn Gly Leu Ala Pro Phe Thr Leu
 405 410 415
 Glu Thr Ser Gly Trp Asn Gly Thr Asp Val Ser Leu Glu Gly Lys Phe
 420 425 430
 Gln Met Glu Asp Leu Val Tyr Asn Pro Glu Gln Val Pro Arg Tyr Tyr
 435 440 445
 Gln Asn Ala Tyr Leu His Leu Arg Pro Phe Tyr Ser Thr Thr Arg Ser
 450 455 460
 Phe Leu Gly Ile His Arg Leu Asn Gly Pro Leu Lys Cys Gly Gln Pro
 465 470 475 480
 Gln Glu Val Leu Val Asp Tyr Tyr Ile Asp Pro Ala Asp Ala Ser Pro
 485 490 495
 Asp Gln Glu Ile Ser Phe Ser Tyr Tyr Leu Ile Gly Lys Gly Ser Leu
 500 505 510

Cura 468 SEQ list 0705

Val	Met	Glu	Gly	Gln	Lys	His	Leu	Asn	Ser	Lys	Lys	Lys	Gly	Leu	Lys
	515						520					525			
Ala	Ser	Phe	Ser	Leu	Ser	Leu	Thr	Phe	Thr	Ser	Arg	Leu	Ala	Pro	Asp
	530					535					540				
Pro	Ser	Leu	Val	Ile	Tyr	Ala	Ile	Phe	Pro	Ser	Gly	Gly	Val	Val	Ala
545					550					555					560
Asp	Lys	Ile	Gln	Phe	Ser	Val	Glu	Met	Cys	Phe	Asp	Asn	Gln	Gln	Leu
				565					570					575	
Pro	Gly	Ala	Glu	Val	Glu	Leu	Gln	Leu	Gln	Ala	Ala	Pro	Gly	Ser	Leu
			580					585					590		
Cys	Ala	Leu	Arg	Ala	Val	Asp	Glu	Ser	Val	Leu	Leu	Leu	Arg	Pro	Asp
		595					600					605			
Arg	Glu	Leu	Ser	Asn	Arg	Ser	Val	Tyr	Gly	Met	Phe	Pro	Phe	Trp	Tyr
	610					615					620				
Gly	His	Tyr	Pro	Tyr	Gln	Val	Ala	Glu	Tyr	Asp	Gln	Cys	Pro	Val	Ser
625					630					635					640
Gly	Pro	Trp	Asp	Phe	Pro	Gln	Pro	Leu	Ile	Asp	Pro	Met	Pro	Gln	Gly
				645					650					655	
His	Ser	Ser	Gln	Arg	Ser	Ile	Ile	Trp	Arg	Pro	Ser	Phe	Ser	Glu	Gly
			660					665					670		
Thr	Asp	Leu	Phe	Ser	Phe	Phe	Arg	Asp	Val	Gly	Leu	Lys	Ile	Leu	Ser
		675					680					685			
Asn	Ala	Lys	Ile	Lys	Lys	Pro	Val	Asp	Cys	Ser	His	Arg	Ser	Pro	Glu
	690					695					700				
Tyr	Ser	Thr	Ala	Met	Gly	Gly	Gly	Gly	His	Pro	Glu	Ala	Phe	Glu	Ser
705					710					715					720
Ser	Thr	Pro	Leu	His	Gln	Ala	Glu	Asp	Ser	Gln	Val	Arg	Gln	Tyr	Phe
				725					730					735	
Pro	Glu	Thr	Trp	Leu	Trp	Asp	Leu	Phe	Pro	Ile	Gly	Asn	Ser	Gly	Lys
			740					745					750		
Glu	Ala	Val	His	Val	Thr	Val	Pro	Asp	Ala	Ile	Thr	Glu	Trp	Lys	Ala
		755					760					765			
Met	Ser	Phe	Cys	Thr	Ser	Gln	Ser	Arg	Gly	Phe	Gly	Leu	Ser	Pro	Thr
	770					775					780				
Val	Gly	Leu	Thr	Ala	Phe	Lys	Pro	Phe	Phe	Val	Asp	Leu	Thr	Leu	Pro
785					790					795					800
Tyr	Ser	Val	Val	Arg	Gly	Glu	Ser	Phe	Arg	Leu	Thr	Ala	Thr	Ile	Phe
				805					810					815	
Asn	Tyr	Leu	Lys	Asp	Cys	Ile	Arg	Val	Gln	Thr	Asp	Leu	Ala	Lys	Ser
			820					825					830		
His	Glu	Tyr	Gln	Leu	Glu	Ser	Trp	Ala	Asp	Ser	Gln	Thr	Ser	Ser	Cys
		835					840					845			

Cura 468 SEQ list 0705

Leu Cys Ala Asp Asp Ala Lys Thr His His Trp Asn Ile Thr Ala Val
 850 855 860
 Lys Leu Gly His Ile Asn Phe Thr Ile Ser Thr Lys Ile Leu Asp Ser
 865 870 875 880
 Asn Glu Pro Cys Gly Gly Gln Lys Gly Phe Val Pro Gln Lys Gly Arg
 885 890 895
 Ser Asp Thr Leu Ile Lys Pro Val Leu Val Lys Pro Glu Gly Val Leu
 900 905 910
 Val Glu Lys Thr His Ser Ser Leu Leu Cys Pro Lys Gly Gly Lys Val
 915 920 925
 Ala Ser Glu Ser Val Ser Leu Glu Leu Pro Val Asp Ile Val Pro Asp
 930 935 940
 Ser Thr Lys Ala Tyr Val Thr Val Leu Gly Asp Ile Met Gly Thr Ala
 945 950 955 960
 Leu Gln Asn Leu Asp Gly Leu Val Gln Met Pro Ser Gly Cys Gly Glu
 965 970 975
 Gln Asn Met Val Leu Phe Ala Pro Ile Ile Tyr Val Leu Gln Tyr Leu
 980 985 990
 Glu Lys Ala Gly Leu Leu Thr Glu Glu Ile Arg Ser Arg Ala Val Gly
 995 1000 1005
 Phe Leu Glu Ile Gly Tyr Gln Lys Glu Leu Met Tyr Lys His Ser Asn
 1010 1015 1020
 Gly Ser Tyr Ser Ala Phe Gly Glu Arg Asp Gly Asn Gly Asn Thr Trp
 1025 1030 1035 1040
 Leu Thr Ala Phe Val Thr Lys Cys Phe Gly Gln Ala Gln Lys Phe Ile
 1045 1050 1055
 Phe Ile Asp Pro Lys Asn Ile Gln Asp Ala Leu Lys Trp Met Ala Gly
 1060 1065 1070
 Asn Gln Leu Pro Ser Gly Cys Tyr Ala Asn Val Gly Asn Leu Leu His
 1075 1080 1085
 Thr Ala Met Lys Gly Gly Val Asp Asp Glu Val Ser Leu Thr Ala Tyr
 1090 1095 1100
 Val Thr Ala Ala Leu Leu Glu Met Gly Lys Asp Val Asp Asp Pro Met
 1105 1110 1115 1120
 Val Ser Gln Gly Leu Arg Cys Leu Lys Asn Ser Ala Thr Ser Thr Thr
 1125 1130 1135
 Asn Leu Tyr Thr Gln Ala Leu Leu Ala Tyr Ile Phe Ser Leu Ala Gly
 1140 1145 1150
 Glu Met Asp Ile Arg Asn Ile Leu Leu Lys Gln Leu Asp Gln Gln Ala
 1155 1160 1165
 Ile Ile Ser Gly Glu Ser Ile Tyr Trp Ser Gln Lys Pro Thr Pro Ser
 1170 1175 1180

Cura 468 SEQ list 0705

Ser Asn Ala Ser Pro Trp Ser Glu Pro Ala Ala Val Asp Val Glu Leu
1185 1190 1195 1200

Thr Ala Tyr Ala Leu Leu Ala Gln Leu Thr Lys Pro Ser Leu Thr Gln
1205 1210 1215

Lys Glu Ile Ala Lys Ala Thr Ser Ile Val Ala Trp Leu Ala Lys Gln
1220 1225 1230

His Asn Ala Tyr Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala
1235 1240 1245

Leu Gln Ala Leu Ala Lys Tyr Ala Thr Thr Ala Tyr Met Pro Ser Glu
1250 1255 1260

Glu Ile Asn Leu Val Val Lys Ser Thr Glu Asn Phe Gln Arg Thr Phe
1265 1270 1275 1280

Asn Ile Gln Ser Val Asn Arg Leu Val Phe Gln Gln Asp Thr Leu Pro
1285 1290 1295

Asn Val Pro Gly Met Tyr Thr Leu Glu Ala Ser Gly Gln Gly Cys Val
1300 1305 1310

Tyr Val Gln Thr Val Leu Arg Tyr Asn Ile Leu Pro Pro Thr Asn Met
1315 1320 1325

Lys Thr Phe Ser Leu Ser Val Glu Ile Gly Lys Ala Arg Cys Glu Gln
1330 1335 1340

Pro Thr Ser Pro Arg Ser Leu Thr Leu Thr Ile His Thr Ser Tyr Val
1345 1350 1355 1360

Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu
1365 1370 1375

Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln
1380 1385 1390

Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr
1395 1400 1405

Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser
1410 1415 1420

Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr
1425 1430 1435 1440

Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val
1445 1450 1455

Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro
1460 1465 1470

Glu Pro Pro Pro Phe Lys Thr Glu Ala Phe Ile Pro Ser Leu Pro Gly
1475 1480 1485

Ser Val Asn Asn
1490

<210> 11
<211> 987

Cura 468 SEQ list 0705

<212> DNA

<213> Homo sapiens

<400> 11

```

atgagagcca attgttccag cagctcagcc tgccctgcca acagttcaga ggaggagctg 60
ccagtgggac tggaggtgca tggaaacctg gagctcgttt tcacagtggg gtccactatc 120
atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtggtcg 180
cacatcagga gaccctgggg cattgctgtg ggactgctct gccagtttgg gctcatgcct 240
tttacagctt atctcctggc cattagcttt tctctgaagc cagtccaagc tattgctgtt 300
ctcatcatgg gctgctgccg gggggcacca tctctaacad tttcaccttc tgggttgatg 360
gagatatgga tctcaggtgc cctgggaatg atgccactct gcatttatct ctacacctgg 420
tcttgagtc ttcagcagaa tctcaccatt ccttatcaga acataggctt gtcttttagga 480
attacccttg tgtgcctgac cattcctgtg gcctttgggt tctatgtgaa ttacagatgg 540
ccaaaacaat ccaaaatcat tctcaaggcc gttgttggtg gggtcctcct tctggtggtc 600
gcagttgctg gtgtgggtcct ggcgaaagga tcttggaatt cagacatcac ccttctgacc 660
atcagtttca tctttccttt gattggccat gtcacgggtt ttctgctggc actttttacc 720
caccagtctt ggcaaaggac cttgcctatc tttttaggtt tagctttcaa gacacctgt 780
gataccctac tcgcaatgac ttcgtgtcct gaatgttcca ggctcatcta tgccttcatt 840
cctctgctat atggactctt ccagctgata gatggatttc ttattgttga agagagaaca 900
gaagatacag actgcgatgg ttcaccttta cctgagtatt ttactgaggt aacaataata 960
cctaaacaac ctaggatatg acagctt 987

```

<210> 12

<211> 326

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Arg Ala Asn Cys Ser Ser Ser Ser Ala Cys Pro Ala Asn Ser Ser
 1              5              10              15

Glu Glu Glu Leu Pro Val Gly Leu Glu Val His Gly Asn Leu Glu Leu
      20              25              30

Val Phe Thr Val Val Ser Thr Ile Met Met Gly Leu Leu Met Phe Ser
      35              40              45

Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg
      50              55              60

Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro
      65              70              75              80

Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
      85              90              95

Ala Ile Ala Val Leu Ile Met Gly Cys Cys Arg Gly Ala Pro Ser Leu
      100              105              110

Thr Phe Ser Pro Ser Gly Leu Met Glu Ile Trp Ile Ser Gly Ala Leu
      115              120              125

Gly Met Met Pro Leu Cys Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu
      130              135              140

Gln Gln Asn Leu Thr Ile Pro Tyr Gln Asn Ile Gly Leu Ser Leu Gly
      145              150              155              160

Ile Thr Leu Val Cys Leu Thr Ile Pro Val Ala Phe Gly Val Tyr Val
      165              170              175

Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile Ile Leu Lys Ala Val Val

```

Cura 468 SEQ list 0705
185 190

180
Gly Gly Val Leu Leu Leu Val Val Ala Val Ala Gly Val Val Leu Ala
195 200 205
Lys Gly Ser Trp Asn Ser Asp Ile Thr Leu Leu Thr Ile Ser Phe Ile
210 215 220
Phe Pro Leu Ile Gly His Val Thr Gly Phe Leu Leu Ala Leu Phe Thr
225 230 235 240
His Gln Ser Trp Gln Arg Thr Leu Pro Ile Phe Leu Gly Leu Ala Phe
245 250 255
Lys Thr Pro Cys Asp Thr Leu Leu Ala Met Thr Ser Cys Pro Glu Cys
260 265 270
Ser Arg Leu Ile Tyr Ala Phe Ile Pro Leu Leu Tyr Gly Leu Phe Gln
275 280 285
Leu Ile Asp Gly Phe Leu Ile Val Glu Glu Arg Thr Glu Asp Thr Asp
290 295 300
Cys Asp Gly Ser Pro Leu Pro Glu Tyr Phe Thr Glu Val Thr Ile Ile
305 310 315 320
Pro Lys Gln Pro Arg Ile
325

<210> 13
<211> 850
<212> DNA
<213> Homo sapiens

<400> 13
aaaacatggc tgccaaaatg tttgagttca tcggcaagtt tggcctggcc ttagttgttg 60
caggaggcgt ggtgaactct gccttatata gtgtggatgc tgggcacaga gctgtcgtct 120
ttgaccgatt ccgtggagtg caggacattg tggtaggcaa agggactcac tgtctcatcc 180
catggttaca gaaatcaata atctttgact gccgttctca gccacgtaat gtgccagtca 240
tcaccggtag caaagattta cagaatgtca acctcacact gcgcatcatc ttccggcccg 300
tagctagcca gcttcctcac atcttcacca gcagcggaga ggaccatgat gagcgtgtgc 360
cgccgtccat cacgaacaag atcctcaagt cagtgggtggc tcgctttgaa gctggagaac 420
taatcaccca gagagagcag atctccaggc aggtgagcga tgaccttacg gagccagcag 480
ccaccttttg gctcattctg gacgacgtgt ccttgacata tctgaccttc gggaaggagt 540
tcatagaagc ggtggaagcc aaacagatag ctcagcagga agcagagagg gccagatttg 600
tggtggaaaa ggctgagcag cagaaaaagg cggccatcat ttctgctgag ggcgactcca 660
aggtggccga gctgatcacc aactcactgg ccacagcagg ggacgccctg atcgagctgc 720
gcaagctgga agctgtggag gacatcacct accagctttt acgctctcgg aacatcacct 780
acctgcgggc agggcagtcc atgcccctgc agctgcgctg gtgagggccc accctgcctg 840
cacctccgag 850

<210> 14
<211> 272
<212> PRT
<213> Homo sapiens

<400> 14
Met Ala Ala Lys Met Phe Glu Phe Ile Gly Lys Phe Gly Leu Ala Leu
1 5 10 15
Val Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Ser Val Asp Ala

Cura 468 SEQ list 0705
25 30

20
Gly His Arg Ala Val Val Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
35 40 45
Val Val Gly Lys Gly Thr His Cys Leu Ile Pro Trp Leu Gln Lys Ser
50 55 60
Ile Ile Phe Asp Cys Arg Ser Gln Pro Arg Asn Val Pro Val Ile Thr
65 70 75 80
Gly Ser Lys Asp Leu Gln Asn Val Asn Leu Thr Leu Arg Ile Ile Phe
85 90 95
Arg Pro Val Ala Ser Gln Leu Pro His Ile Phe Thr Ser Ser Gly Glu
100 105 110
Asp His Asp Glu Arg Val Pro Pro Ser Ile Thr Asn Lys Ile Leu Lys
115 120 125
Ser Val Val Ala Arg Phe Glu Ala Gly Glu Leu Ile Thr Gln Arg Glu
130 135 140
Gln Ile Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Pro Ala Ala Thr
145 150 155 160
Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr Leu Thr Phe Gly
165 170 175
Lys Glu Phe Ile Glu Ala Val Glu Ala Lys Gln Ile Ala Gln Gln Glu
180 185 190
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
195 200 205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Val Ala Glu Leu Ile
210 215 220
Thr Asn Ser Leu Ala Thr Ala Gly Asp Ala Leu Ile Glu Leu Arg Lys
225 230 235 240
Leu Glu Ala Val Glu Asp Ile Thr Tyr Gln Leu Leu Arg Ser Arg Asn
245 250 255
Ile Thr Tyr Leu Arg Ala Gly Gln Ser Met Pro Leu Gln Leu Arg Trp
260 265 270

<210> 15
<211> 2011
<212> DNA
<213> Homo sapiens

<400> 15
atggggtggc tcccactcct gctgcttctg actcaatgct taggggtccc tggtcagcgc 60
tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct gctacatgcg 120
gtggtgcccc ggccttggca ggaggatgtg gcagatgctg aagagtgtgc tggtcgctgt 180
gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaactg 240
ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg ctgtgacctc 300
ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg gtaccggggc 360

Cura 468 SEQ list 0705

```

accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa gttcccaaat 420
gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct 480
gatggcgacc ccggaggtcc ctggtgctac acaacagacc ctgctgtgcg cttccagagc 540
tgcggcatca aatcctgccg ggaggccgcg tgtgtctggt gcaatggcga ggaataccgc 600
ggcgcggtag accgcacgga gtcagggcgc gagtgccagc gctgggatct tcagcaccgc 660
caccagcacc ccttcgagcc gggcaagttc ctcgaccaag gtctggacga caactattgc 720
cggaatcctg acggctccga gcggccatgg tgctacacta cggatccgca gatcgagcga 780
gagttctgtg acctcccccg ctgcggttcc gaggcacagc cccgccaaga ggccacaact 840
gtcagctgct tccgcgggaa gggtgagggc taccggggca cagccaatac caccaccgcg 900
ggcgtacctt gccagcgttg ggacgcgcaa atcccgcatc agcaccgatt tacgccagaa 960
aaatacgctt gcaaggacct tcgggagaaac ttctgccgga accccgacgg ctcagaggcg 1020
ccctggtgct tcacactgcg gcccgcatg cgcgcgccct tttgctacca gatccggcgt 1080
tgtacagacg acgtgcggcc ccagactgct accacggcgc aggggagcag taccgcggca 1140
cggtcagcaa gacccgcaag ggtgtccagt gccagcgtg gtccgctgag acgccgcaca 1200
agccgcagtt cacgtttacc tccgaaccgc atgcacaact ggaggagaac ttctgccgga 1260
acccagatgg ggatagccat gggccctggt gctacacgat ggacccaagg accccattcg 1320
actactgtgc cctgcgacgc tgcgctgatg accagccgcc atcaatcctg gacccccag 1380
accaggtgca gtttgagaag tgtggcaaga ggggtggatcg gctggatcag cggcgttcca 1440
agctgcgcgt ggttgggggc catccgggca actcaccctg gacagtcagc ttgcggaatc 1500
ggtatgctgc ctctcacggg ctatgaggta tggttgggca ccctgttcca gaaccacag 1560
catggagagc caagcctaca gcgggtccca gtagccaaga tgggtgtgtg gccctcaggc 1620
tcccagcttg tcctgctcaa gctggagaga tctgtgacct tgaaccagcg tgtggccctg 1680
atctgcctgc cccctgaatg gtatgtggtg cctccaggga ccaagtgtga gattgcaggc 1740
tggggtgaga ccaaaggtag gggtaatgac acagtcctaa atgtggcctt gctgaatgtc 1800
atctccaacc aggagtgtaa catcaagcac cgaggacgtg gtgactacgg gggccactt 1860
gcctgcttta cccacaactg ctgggtcctg gaaggaatta taatcccca cagagtatgc 1920
gcaaggctct gctggccagc tgtcttcacg cgtgtctctg tgtttgtgga ctggattcac 1980
aaggatcatga gactgggtta ggccagcct t 2011

```

<210> 16
 <211> 666
 <212> PRT
 <213> Homo sapiens

<400> 16

```

Met Gly Trp Leu Pro Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
  1           5           10           15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
          20           25           30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
          35           40           45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
          50           55           60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
          65           70           75           80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
          85           90           95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
          100          105          110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
          115          120          125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
          130          135          140

```

Cura 468 SEQ list 0705

Thr 145	Pro	Thr	Leu	Arg	Asn 150	Gly	Leu	Glu	Glu	Asn 155	Phe	Cys	Arg	Asn	Pro 160
Asp	Gly	Asp	Pro	Gly 165	Gly	Pro	Trp	Cys	Tyr 170	Thr	Thr	Asp	Pro	Ala 175	Val
Arg	Phe	Gln	Ser 180	Cys	Gly	Ile	Lys	Ser 185	Cys	Arg	Glu	Ala	Ala 190	Cys	Val
Trp	Cys	Asn 195	Gly	Glu	Glu	Tyr	Arg 200	Gly	Ala	Val	Asp	Arg 205	Thr	Glu	Ser
Gly 210	Arg	Glu	Cys	Gln	Arg	Trp 215	Asp	Leu	Gln	His	Pro 220	His	Gln	His	Pro
Phe 225	Glu	Pro	Gly	Lys	Phe 230	Leu	Asp	Gln	Gly	Leu 235	Asp	Asp	Asn	Tyr	Cys 240
Arg	Asn	Pro	Asp	Gly 245	Ser	Glu	Arg	Pro	Trp 250	Cys	Tyr	Thr	Thr	Asp 255	Pro
Gln	Ile	Glu	Arg 260	Glu	Phe	Cys	Asp	Leu 265	Pro	Arg	Cys	Gly	Ser 270	Glu	Ala
Gln	Pro	Arg 275	Gln	Glu	Ala	Thr	Thr 280	Val	Ser	Cys	Phe	Arg 285	Gly	Lys	Gly
Glu	Gly 290	Tyr	Arg	Gly	Thr	Ala 295	Asn	Thr	Thr	Thr	Ala 300	Gly	Val	Pro	Cys
Gln 305	Arg	Trp	Asp	Ala	Gln 310	Ile	Pro	His	Gln	His 315	Arg	Phe	Thr	Pro	Glu 320
Lys	Tyr	Ala	Cys	Lys 325	Asp	Leu	Arg	Glu	Asn 330	Phe	Cys	Arg	Asn	Pro 335	Asp
Gly	Ser	Glu	Ala 340	Pro	Trp	Cys	Phe	Thr 345	Leu	Arg	Pro	Gly	Met 350	Arg	Ala
Ala	Phe	Cys 355	Tyr	Gln	Ile	Arg	Arg 360	Cys	Thr	Asp	Asp	Val 365	Arg	Pro	Gln
Thr	Ala 370	Thr	Thr	Ala	Gln	Gly 375	Ser	Ser	Thr	Ala	Ala 380	Arg	Ser	Ala	Arg
Pro 385	Ala	Arg	Val	Ser	Ser 390	Ala	Ser	Ala	Gly	Pro 395	Leu	Arg	Arg	Arg	Thr 400
Ser	Arg	Ser	Ser	Arg 405	Leu	Pro	Pro	Asn	Arg 410	Met	His	Asn	Trp	Arg 415	Arg
Thr	Ser	Ala	Gly 420	Thr	Gln	Met	Gly	Ile 425	Ala	Met	Gly	Pro	Gly 430	Ala	Thr
Arg	Trp	Thr 435	Gln	Gly	Pro	His	Ser 440	Thr	Thr	Val	Pro	Cys 445	Asp	Ala	Ala
Leu	Met 450	Thr	Ser	Arg	His	Gln 455	Ser	Trp	Thr	Pro	Gln 460	Thr	Arg	Cys	Ser
Leu 465	Arg	Ser	Val	Ala	Arg 470	Gly	Trp	Ile	Gly	Trp 475	Ile	Ser	Gly	Val	Pro 480

Cura 468 SEQ list 0705

Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser
485 490 495

Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu
500 505 510

Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg
515 520 525

Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val
530 535 540

Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu
545 550 555 560

Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys
565 570 575

Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val
580 585 590

Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile
595 600 605

Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr
610 615 620

His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys
625 630 635 640

Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val
645 650 655

Asp Trp Ile His Lys Val Met Arg Leu Gly
660 665

<210> 17
<211> 634
<212> DNA
<213> Homo sapiens

<400> 17
caagctgccc acgccgacgg caaccctgct ctgcatgccc gcccgcccgt gccaccatg 60
gccacagttc agcagctggg aggaagatgg cgcctggtgg acagcaaacg ctttgatgaa 120
tacatgaagg agggaggagt gggaaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180
gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300
actcagactg tgtgcagctt tgcagatggg gcattgggtc agcatcagga gtgggatggg 360
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtgggtgta ctgtgtcatg 420
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480
ggacaggagt taactaatag aatgatcaag ctcagttcaa tgagcaaadc tccatagtgt 540
tttttttcat tactgtgttc aattatcttt atcacaaacg tttcacatgc agctatttca 600
aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18
<211> 134
<212> PRT
<213> Homo sapiens

<400> 18
Met Ala Thr Val Gln Gln Leu Gly Gly Arg Trp Arg Leu Val Asp Ser

Cura 468 SEQ list 0705

1 5 10 15
 Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu
 20 25 30
 Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe
 50 55 60
 Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg
 65 70 75 80
 Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His
 85 90 95
 Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp
 100 105 110
 Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg
 115 120 125
 Ile Tyr Glu Lys Val Glu
 130

<210> 19
 <211> 822
 <212> DNA
 <213> Homo sapiens

<400> 19
 catgaactgg gcatttctgc agggcctgct gagtggcgtg aacaagtact ccacagtgct 60
 gagccgcatc tggctgtctg tgggtgttcat ctttcgtgtg ctggtgtacg tgggtggcagc 120
 ggaggagggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggctg 180
 ccccaacgtc tgctatgacg agttcttccc cgtgtccac gtgcgcctct gggccctaca 240
 gctcatcctg gtcacgtgcc cctcactgct cgtggtcatg cacgtggcct accgcgagga 300
 acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360
 gagcaagaag cggggcggac tgtggtggac gtacttgctg agcctcatct tcaaggccgc 420
 cgtggatgct ggcttctctt atatcttcca ccgcctctac aaggattatg acatgccccg 480
 cgtggtggcc tgctccgtgg agccttgccc ccacactgtg gactgttaca tctcccggcc 540
 cacggagaag aaggtcttca cctacttcat ggtgaccaca gctgccatct gcatcctgct 600
 caacctcagt gaagtcttct acctggtggg caagagggtg atggagatct tcggccccag 660
 gcaccggcgg cctcgggtgcc gggaaatgcct acccgatacg tgcccaccat atgtcctctc 720
 ccagggaggg caccctgagg atgggaactc tgtcctaata aaggctgggt cggccccagt 780
 ggatgcaggt gggatatccat aacctgcgag atcagcagat aa 822

<210> 20
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30
 val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45

Cura 468 SEQ list 0705

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
130 135 140
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
210 215 220
Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
225 230 235 240
Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
245 250 255
Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
260 265

<210> 21
<211> 546
<212> DNA
<213> Homo sapiens

<400> 21
caatctgaca tgtaactgta aaatcactgg gcccgaggag tgactgtaat taagggctta 60
cgttgaaaat gtataaacag agcttgattc ttaagtttcg aaaattcttc acagtgatgg 120
tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaga aagccacttc 180
aggaaatacc acggtcacac ctgagttggc ttcattgctac agattataga aaatatgttg 240
ctgcccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300
gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360
agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420
cttttagtac tgacattctg gatttttaaaa gttatgttga ccgcatgttc tcactcacia 480
gtgggagttg aacaatgaga acacacggac acggggaagg gaacatcaca caccagggcc 540
tgtcag 546

<210> 22

Cura 468 SEQ list 0705

<211> 61
<212> PRT
<213> Homo sapiens

<400> 22
Met Leu Gln Ile Ile Glu Asn Met Leu Leu Pro Gly Pro Pro Ile Cys
1 5 10 15
Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile
20 25 30
His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val
35 40 45
Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser
50 55 60

<210> 23
<211> 2309
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (2196)
<223> wherein n is an a o t or c or g.

<400> 23
gagtgaagagg tcggacagac tgtggagccg acagactgaa ggacagcggc accgccagac 60
ggccagaaag ttccgccatg agctggggca cggagctgtg ggatcagttc gacagcttag 120
acaagcatac acaatgggga attgacttct tggaaagata tgccaaattt gttaaagaga 180
ggatagaaat tgaacagaac tatgcgaaac aattgagaaa tctgggtaag aagtactgcc 240
ccaaacgttc atccaaagat gaagagccac ggtttacctc gtgtgttagcc ttttttaata 300
tccttaatga gttaaatgac tatgcaggac agcgagaagt tgtagcagaa gaaatggcgc 360
acagagtgtg tgggtgaatta atgagatatg ctcatgatct gaaaactgaa agaaaaatgc 420
atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaaa cagatgggta 480
atagtaaaaa gaagtttgaa agagaatgta gagaggcaga aaaggcacia cagagttatg 540
aaagattgga taatgatact aatgcaacca aggcagatgt tgaaaatgcc aaacagcagt 600
tgaatctgcg tacgcatatg gccgatgaaa ataaaaatgc atatgctgca caattacaaa 660
actttaatgg agaacaacat aaacattttt atgtagtgtat tcctcagatt tacaagcaac 720
tacaagaaat ggacgaacga aggactatta aactcagtga gtgttacaga ggatttgctg 780
actcagaacg caaagttatt cccatcattt caaaatgttt ggaaggaatg attcttgtag 840
caaaatcagt tgatgaaaga agagactctc aaatgggtgg agactccttc aaatctgggt 900
ttgaacctcc aggagacttt ccatttgaag attacagtca acatatatat agaaccattt 960
ctgatgggac tatcagtgca tccaaacagg agagtgggaa gatggatgcc aaaaccccag 1020
taggaaaggc caagggcaaa ttgtggctct ttggaaagaa gccaaagggc ccagcactag 1080
aagatttcag tcattctgcca ccagaacaga gacgtaaaaa actacagcag cgcattgatg 1140
aacttaacag agaactacag aaagaatcag accaaaaaga tgcactcaac aaaatgaaag 1200
atgtatatga gaaggatcca caaatggggg atccagggag tttgcagcct aaattagcag 1260
agaccatgaa taacattgac cgcctacgaa tggaaatcca taagaatgag gcttggctct 1320
ctgaagtcga aggcaaaaca ggtgggagag gagacagaag acatagcagt gacataaatc 1380
atcttgaac acagggacga gaaagtcctg aggggaagtta cactgatgat gcaaaccagg 1440
aagtccgtgg gccaccccag cagcatgggt accacaatga gtttgatgat gaatttgagg 1500
atgatgatcc cttgcctgct attggacact gcaaagctat ctaccctttt gatggacata 1560
atgaaggtag tctagcaatg aaagaagggt aagttctcta cattatagag gaggacaaag 1620
gtgacggatg gacaagagct cggagacaga acggtgaaga aggctacgtt cccacgtcat 1680
acatagatgt aactctagag aaaaacagta aaggttcctg aagaggggtt ctgaggaaat 1740
gggcaagatg ttgaaggagg ttacatgcag ctgctttttg gggaggggtat tagagttgtc 1800
aggctcaaag agagtgaag aagcaagttg catgagtgca tgcagacatg attttttttt 1860
tactaacttc attagcattt ccatacattg tttttaaaaa tcataataacc aacccttaag 1920
ttcctagttc acagttattt ccacaaaaga aaaagccaac aatagtgtac catttttcta 1980
ttttatttta ttgctgtcta atcaataaag aatgcagagc tgtcaaaaaa tgtgtcttac 2040

Cura 468 SEQ list 0705

```

atttagctgt cccaacagga ttgtcttccc tcccagctct gggttttaatt ggcttttaga 2100
cccactatct gtcagatcct tgccatctgt cagtgtctgc ctgcccacc tccgtgcttg 2160
cctaacatcc tgttgcatgt ctacgctgat tgagcnagat tttcaggcat gtccttagaa 2220
tcccctggtn ctgtcaaagc ctggtttggt ttacattggt ngtgcaatcn ctttgtcaac 2280
atctccagca ctatngttcc ntcttaggt 2309

```

<210> 24
 <211> 547
 <212> PRT
 <213> Homo sapiens

<400> 24

```

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys
  1          5          10          15
His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val
          20          25          30
Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn
          35          40          45
Leu Val Lys Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro
          50          55          60
Arg Phe Thr Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn
          65          70          75          80
Asp Tyr Ala Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg
          85          90          95
Val Tyr Gly Glu Leu Met Arg Tyr Ala His Asp Leu Lys Thr Glu Arg
          100          105          110
Lys Met His Leu Gln Glu Gly Arg Lys Ala Gln Gln Tyr Leu Asp Met
          115          120          125
Cys Trp Lys Gln Met Gly Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys
          130          135          140
Arg Glu Ala Glu Lys Ala Gln Gln Ser Tyr Glu Arg Leu Asp Asn Asp
          145          150          155          160
Thr Asn Ala Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn
          165          170          175
Leu Arg Thr His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln
          180          185          190
Leu Gln Asn Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile
          195          200          205
Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile
          210          215          220
Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val
          225          230          235          240
Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys
          245          250          255
Ser Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys
          260          265          270

```


Cura 468 SEQ list 0705

Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln
275 280 285
His Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser Lys Gln
290 295 300
Glu Ser Gly Lys Met Asp Ala Lys Thr Pro Val Gly Lys Ala Lys Gly
305 310 315 320
Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys Gly Pro Ala Leu Glu Asp
325 330 335
Phe Ser His Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg
340 345 350
Ile Asp Glu Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp
355 360 365
Ala Leu Asn Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly
370 375 380
Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile
385 390 395 400
Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu
405 410 415
Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp
420 425 430
Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr
435 440 445
Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly
450 455 460
His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro
465 470 475 480
Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu
485 490 495
Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu
500 505 510
Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu
515 520 525
Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser
530 535 540
Lys Gly Ser
545

<210> 25

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 25

gcggaacatt gcctagtaga ccctgaggct ttacaacagt gccactgacc cctatgagcc 60

Cura 468 SEQ list 0705

tgatgctgga	tgaccaaccc	cctatggagg	cccagtatgc	agaggagggc	ccaggacctg	120
ggatcttcag	agcagagcct	ggagaccagc	agcatcccat	ttctcaggcg	gtgtgctggc	180
gttccatgcg	acgtggctgt	gcagtgctgg	gagccctggg	gctgctggcc	ggtgcaggtg	240
ttggctcatg	gctcctagtg	ctgtatctgt	gtcctgctgc	ctctcagccc	atttccggga	300
ccttgcagga	tgaggagata	actttgagct	gctcagaggc	cagcgctgag	gaagctctgc	360
tccctgcact	tcccaaaaca	gtatctttca	gaataaacag	cgaagacttc	ttgctggaag	420
cgcaagtga	ggatcagcca	cgctggctcc	tggtctgcca	tgagggctgg	agccccgccc	480
tggggctgca	gatctgctgg	agccttgggc	atctcagact	cactcaccac	aaggagtaa	540
acctcactga	catcaaactc	aacagtcccc	aggagtctgc	tcagctctct	cctagactgg	600
gaggcttcct	ggaggaggcg	tggcagccca	gtaggactac	tgaggctgtt	aggaacaact	660
gcacttctgg	tcaagtgtgt	tccctcagat	gctctgagtg	tggagcgagg	cccctggctt	720
cccggatagt	tggtgggcag	tctgtggctc	ctgggcgctg	gccgtggcag	gccagcgtgg	780
ccctgggctt	ccggcacacg	tgtgggggct	ctgtgctagc	gccacgctgg	gtggtgactg	840
ctgcacattg	tatgcacagt	ttcaggctgg	cccgcctgtc	cagctggcgg	gttcatgcgg	900
ggctggctcag	ccacagtgcc	gtcaggcccc	accaaggggc	tctgggtggag	aggattatcc	960
cacacccccct	ctacagtgcc	cagaatcatg	actacgacgt	cgccctcctg	aggctccaga	1020
ccgctctcaa	cttctcagac	actgtgggcg	ctgtgtgcct	gccggccaag	gaacagcatt	1080
ttccgaaggg	ctcgcggtgc	tgggtgtctg	gctggggcca	caccacccct	agccatactt	1140
acagctcgga	tatgctccag	gacacggtgg	tgccccctgct	cagcactcag	ctctgcaaca	1200
gctcttgctg	gtacagcgga	gccctcacc	cccgcctgct	ttgcgctggc	tacctggacg	1260
gaagggtgta	tgcattgccag	ggagatagcg	ggggccccct	agtgtgcca	gatggggaca	1320
catggcgctt	agtgggggtg	gtcagctggg	ggcgtggctg	cgcagagccc	aatcacccag	1380
gtgtctacgc	caaggtagct	gagtttctgg	actggatcca	tgacactgct	caggtgagtg	1440
tgggggacag	agtagggcag	ggagatttct	aaaggacctg	ccctcgaatg	caaggaacct	1500
taccccttag	gcccgggccc	tgctggggac	tggggagggt	gctaggacat	attccccaga	1560
gtgagtggag	gaagaagtga	agcttaaaca	tggaatccat	tggatttcta	tcagtttaag	1620
gatgaactgg	gtaagagtat	gcctgagttt	gtatcccaga	tctaccattt	cctgtgtcga	1680
cctttggcaa	atttctaact	ttgttaaacc	ttaatttcct	gataataacc	atgatggcta	1740
cttatatgct	attgttatat	gctattaaat	aagaccgcta	caatgcc		1787

<210> 26

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 26

ggcattgtac	gggtcttatt	taatagcata	taacaatagc	atataagtag	ccatcatggt	60
tattatcagg	aaattaaggt	ttaacaaagt	tagaaatttg	ccaaaggctc	acacaggaaa	120
tggtagatct	gggatacaaa	ctcaggcata	ctcttacc	gttcatcctt	aaactgatag	180
aaatccaatg	gattccatgt	ttaagcttca	cttcttcctc	cactcactct	ggggaatatg	240
tcctagcacc	ctccccagtc	cccagcaggg	cccgggccta	aggggtaagg	ttccttgc	300
tcgagggcag	gtcctttaga	aatctccctg	ccctactcct	gccccacac	tcacctgagc	360
agtgtcatgg	atccagtcca	gaaactcagc	taccttggcg	tagacacctg	ggtgattggg	420
ctctgcgag	ccacgcccc	agctgaccac	ccccactagg	cgccatgtgt	ccccatctgg	480
gcacactagg	gggcccccg	tatctccctg	gcatgcatca	gcccttcctg	ccaggtagcc	540
agcgcaaagc	atgcgggggg	tgagggctcc	gctgtacacg	caagagctgt	tgcagagctg	600
agtgtgagc	aggggcacca	ccgtgtcctg	gagcatatcc	gagctgtaag	tatggctagg	660
gtgggtgtgg	ccccagccag	acacccagca	ccgcgagccc	ttcggaatat	gctgttcctt	720
ggccggcagg	cacacagcgc	ccacagtgtc	tgagaagttg	agagcggctc	ggagcctcag	780
gagggcgacg	tcgtagtcat	gattctgggc	actgtagagg	gggtgtggga	taatcctctc	840
caccagagcc	ccttgggtgg	gcctgacggc	actgtggctg	accagccccg	catgaacccg	900
ccagctggac	aggcggggcca	gcctgaaact	gtgcatacaa	tgtgcagcag	tcaccacca	960
gcgtggcgct	agcacagagc	ccccacacgt	gtgccggaag	cccagggcca	cgctggcctg	1020
ccacggccag	cgcccaggag	ccacagactg	cccaccaact	atccgggaag	ccaggggcct	1080
cgctccacac	tcagagcatc	tgagggaac	aacttgacca	gaagtgcagt	tgttccta	1140
agcctcagta	gtcctactgg	gctgccacgc	ctcctccagg	aagcctccca	gtctaggaga	1200
gagctgagca	aactcctggg	aactgttgag	tttgatgtca	gtgaggttta	ctcccttg	1260
gtgagtga	ctgagatgcc	caaggctcca	gcagatctgc	agccccagg	cggggctcca	1320
gccctcatgg	cagaccagga	gccagcgtgg	ctgatccctc	acttgcgctt	ccagcaagaa	1380
gtcttcgctg	tttattctga	aagatactgt	tttgggaagt	gcaggagca	gagcttcctc	1440
agcgctggcc	tctgagcagc	tcaaagtatt	ctcctcatcc	tgcaaggctc	cggaaatggg	1500
ctgagaggca	gcaggacaca	gatacagcac	taggagccat	gagccaacac	ctgcaccggc	1560

Cura 468 SEQ list 0705

cagcagcccc agggctccca gcactgcaca gccacgtcgc atggaacgcc agcacaccgc 1620
 ctgagaaatg ggatgctgct ggtctccagg ctctgctctg aagatcccag gtcctggggc 1680
 ctctctgca tactgggcct ccataggggg ttggtcatcc agcatcaggc tcataggggt 1740
 cagtggcact gttgtaaagc ctcaggggtct actaggcaat gttccgc 1787

<210> 27
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15
 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30
 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Ser Arg Thr Thr Glu Ala Val Arg Asn Asn Cys Thr Ser Gly Gln Val
 195 200 205
 Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg
 210 215 220
 Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln Ala
 225 230 235 240
 Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu Ala
 245 250 255
 Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg Leu
 260 265 270

Cura 468 SEQ list 0705

Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Ser
 275 280 285

Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro His
 290 295 300

Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Arg
 305 310 315 320

Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu
 325 330 335

Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val Ser
 340 345 350

Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met Leu
 355 360 365

Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn Ser Ser
 370 375 380

Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr
 385 390 395 400

Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
 405 410 415

Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp
 420 425 430

Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys Val
 435 440 445

Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Val Ser Val Gly
 450 455 460

Ala Gly Val Gly Gln Gly Asp Phe
 465 470

<210> 28
 <211> 2148
 <212> DNA
 <213> Homo sapiens

<400> 28
 acgcgggata cagggagggg ccatgtgcga accagggaga cctcatcttc caaccaagct 60
 tgctgggctt gcatttaatc aatgcatggc cagagaacag gagcgggaaca ttgcctagta 120
 gaccctgagg ctttacaaca gtgctactga cccctatgag cctgatgctg gatgaccaac 180
 cccctatgga ggcccagtat gcagaggagg gcccaggacc tgggatcttc agagcagagc 240
 ctggagacca gcagcatccc atttctcagg cggtgtgctg gcgttccatg cgacgtggct 300
 gtgcagtgtt gggagccctg gggctgctgg ccggtgcagg tgttggtctca tggctcctag 360
 tgctgtatct gtgtcctgct gcctctcagc ccatttccgg gaccttgag gatgaggaga 420
 taactttgag ctgctcagag gccagcgtg aggaagctct gctccctgca ctccccaaaa 480
 cagtatcttt cagaataaac agcgaagact tcttgctgga agcgcaagtg agggatcagc 540
 cacgctggct cctggtctgc catgagggtt ggagccccgc cctggggctg cagatctgct 600
 ggagccttgg gcatctcaga ctactcacc acaaggaggt aaacctcact gacatcaaac 660
 tcaacagttc ccaggagtgt gctcagctct ctctagact gggaggcttc ctggaggagg 720
 cgtggcagcc caggaacaac tgcacttctg gtcaagtgtt ttccctcaga tgctctgagt 780
 gtggagcgag gcccttggtt tcccggatag ttggtgggca gtctgtggct cctgggctgct 840
 ggccgtggca ggccagcgtg gccctgggct tccggcacac gtgtgggggc tctgtgctag 900
 cgccacgctg ggtggtgact gctgcacatt gtatgcacag tgcccagaat catgactacg 960
 acgtcgccct cctgaggctc cagaccgctc tcaacttctc agacactgtg ggcgctgtgt 1020

Cura 468 SEQ list 0705

```

gcctgccggc caaggaacag cattttccga agggctcgcg gtgctgggtg tccggctggt 1080
gccacacca ccctagccat acttacagct cggatatgct ccaggacacg gtggtgcccc 1140
tgctcagcac tcagctctgc aacagctctt gcgtgtacag cggagccctc accccccgca 1200
tgctttgcgc tggctacctg gacggaaggg ctgatgcatg ccaggagat agcgggggcc 1260
ccctagtgtg ccagatggg gacacatggc gcctagtggg ggtggtcagc tgggggcgtg 1320
gctgcgcaga gccaatcac ccagggtgtct acgccaagggt agctgagttt ctggactgga 1380
tccatgacac tgctcaggac tccctcctct gagtcctgct gtttcctcca gtctcactgc 1440
acaccactgc ctcatgcttc ctggggcctc cagcagctcc actaatggag gagaggcagt 1500
agcctccgac acagaacgca tggacctcct actactgtgt gtgaggaaca gtcactaccc 1560
actggccagc caccagcca acaggctctt cctcttgggc cctgatttca gagtcctctt 1620
tctcactaga gactcaatga cagaagagag gctgggactt ggttgggcat gctgtggttg 1680
ctgagggatg agggggagga gagaggtagg agctggagat gaagagactg ctagaagcag 1740
caggaagcct gcccttctgc cctctccctt ccctgcccct gtgtgagctt tttaggagg 1800
gtgactggga ggtgcccccc gtcccacctt tttcctgtgc tctagggtgg ctaagtgcct 1860
ccctagagga ctccatggct gagaggctcc tgggcagatg ggggtcaaggc tgggccagtc 1920
ccagatgaag cctatgggag tcaggacctt ctccactctc cctctccact ccccttcctg 1980
ttctcacctg gctgtggctg gccctgtgtg ggggtgggtac actggaaaac aagaaggttg 2040
gagttggtct aggacattgg ttttaaataga cagttctgtg aactggtcca aggaggttct 2100
gttattaaag tgatatatgg tcttgaaaaa aaaaaaaaaa aaaaaaaa 2148

```

<210> 29

<211> 418

<212> PRT

<213> Homo sapiens

<400> 29

```

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1           5           10           15
Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
           20           25           30
Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
           35           40           45
Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
           50           55           60
Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
           65           70           75           80
Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
           85           90           95
Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
           100          105          110
Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
           115          120          125
Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
           130          135          140
Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
           145          150          155          160
Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
           165          170          175
Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
           180          185          190

```

Cura 468 SEQ list 0705

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
195 200 205
Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
210 215 220
Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
225 230 235 240
His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
245 250 255
Ala His Cys Met His Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu
260 265 270
Leu Arg Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val
275 280 285
Cys Leu Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp
290 295 300
Val Ser Gly Trp Cys His Thr His Pro Ser His Thr Tyr Ser Ser Asp
305 310 315 320
Met Leu Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn
325 330 335
Ser Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala
340 345 350
Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly
355 360 365
Pro Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val
370 375 380
Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala
385 390 395 400
Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser
405 410 415

Leu Leu

<210> 30
<211> 1593
<212> PRT
<213> Homo sapiens

<400> 30
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1 5 10 15
Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
20 25 30
Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
35 40 45
Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
50 55 60

Cura 468 SEQ list 0705

His 65	Phe	Leu	Ser	Tyr	Gly 70	Leu	His	Tyr	Pro	Ile 75	Thr	Ser	Ser	Arg	Arg 80
Lys	Arg	Asp	Leu	Asp 85	Gly	Ser	Glu	Asp	Trp 90	Val	Tyr	Tyr	Arg	Ile 95	Ser
His	Glu	Glu	Lys 100	Asp	Leu	Phe	Phe	Asn 105	Leu	Thr	Val	Asn	Gln 110	Gly	Phe
Leu	Ser	Asn 115	Ser	Tyr	Ile	Met	Glu 120	Lys	Arg	Tyr	Gly	Asn 125	Leu	Ser	His
Val	Lys 130	Met	Met	Ala	Ser	Ser 135	Ala	Pro	Leu	Cys	His 140	Leu	Ser	Gly	Thr
Val 145	Leu	Gln	Gln	Gly	Thr 150	Arg	Val	Gly	Thr	Ala 155	Ala	Leu	Ser	Ala	Cys 160
His	Gly	Leu	Thr	Gly 165	Phe	Phe	Gln	Leu	Pro 170	His	Gly	Asp	Phe	Phe	Ile 175
Glu	Pro	Val	Lys 180	Lys	His	Pro	Leu	Val 185	Glu	Gly	Gly	Tyr	His 190	Pro	His
Ile	Val	Tyr 195	Arg	Arg	Gln	Lys	Val 200	Pro	Glu	Thr	Lys	Glu 205	Pro	Thr	Cys
Gly	Leu 210	Lys	Asp	Ser	Val	Asn 215	Ile	Ser	Gln	Lys	Gln 220	Glu	Leu	Trp	Arg
Glu 225	Lys	Trp	Glu	Arg	His 230	Asn	Leu	Pro	Ser	Arg 235	Ser	Leu	Ser	Arg	Arg 240
Ser	Ile	Ser	Lys	Glu 245	Arg	Trp	Val	Glu	Thr 250	Leu	Val	Val	Ala	Asp 255	Thr
Lys	Met	Ile	Glu 260	Tyr	His	Gly	Ser	Glu 265	Asn	Val	Glu	Ser	Tyr 270	Ile	Leu
Thr	Ile	Met 275	Asn	Met	Val	Thr	Gly 280	Leu	Phe	His	Asn 285	Pro	Ser	Ile	Gly
Asn 290	Ala	Ile	His	Ile	Val	Val 295	Val	Arg	Leu	Ile	Leu 300	Leu	Glu	Glu	Glu
Glu 305	Gln	Gly	Leu	Lys	Ile 310	Val	His	His	Ala	Glu 315	Lys	Thr	Leu	Ser	Ser 320
Phe	Cys	Lys	Trp	Gln 325	Lys	Ser	Ile	Asn	Pro 330	Lys	Ser	Asp	Leu	Asn 335	Pro
Val	His	His	Asp 340	Val	Ala	Val	Leu	Leu 345	Thr	Arg	Lys	Asp	Ile 350	Cys	Ala
Gly	Phe	Asn 355	Arg	Pro	Cys	Glu	Thr 360	Leu	Gly	Leu	Ser	His 365	Leu	Ser	Gly
Met 370	Cys	Gln	Pro	His	Arg	Ser 375	Cys	Asn	Ile	Asn	Glu 380	Asp	Ser	Gly	Leu
Pro 385	Leu	Ala	Phe	Thr	Ile 390	Ala	His	Glu	Leu	Gly 395	His	Ser	Phe	Gly	Ile 400

Cura 468 SEQ list 0705

Gln His Asp Gly Lys Glu Asn Asp Cys Glu Pro Val Gly Arg His Pro
 405 410 415
 Tyr Ile Met Ser Arg Gln Leu Gln Tyr Asp Pro Thr Pro Leu Thr Trp
 420 425 430
 Ser Lys Cys Ser Glu Glu Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp
 435 440 445
 Gly Phe Cys Leu Asp Asp Ile Pro Lys Lys Lys Gly Leu Lys Ser Lys
 450 455 460
 Val Ile Ala Pro Gly Val Ile Tyr Asp Val His His Gln Cys Gln Leu
 465 470 475 480
 Gln Tyr Gly Pro Asn Ala Thr Phe Cys Gln Glu Val Glu Asn Val Cys
 485 490 495
 Gln Thr Leu Trp Cys Ser Val Lys Gly Phe Cys Arg Ser Lys Leu Asp
 500 505 510
 Ala Ala Ala Asp Gly Thr Gln Cys Gly Glu Lys Lys Trp Cys Met Ala
 515 520 525
 Gly Lys Cys Ile Thr Val Gly Lys Lys Pro Glu Ser Ile Pro Gly Gly
 530 535 540
 Trp Gly Arg Trp Ser Pro Trp Ser His Cys Ser Arg Thr Cys Gly Ala
 545 550 555 560
 Gly Val Gln Ser Ala Glu Arg Leu Cys Asn Asn Pro Glu Pro Lys Phe
 565 570 575
 Gly Gly Lys Tyr Cys Thr Gly Glu Arg Lys Arg Tyr Arg Leu Cys Asn
 580 585 590
 Val His Pro Cys Arg Ser Glu Ala Pro Thr Phe Arg Gln Met Gln Cys
 595 600 605
 Ser Glu Phe Asp Thr Val Pro Tyr Lys Asn Glu Leu Tyr His Trp Phe
 610 615 620
 Pro Ile Phe Asn Pro Ala His Pro Cys Glu Leu Tyr Cys Arg Pro Ile
 625 630 635 640
 Asp Gly Gln Phe Ser Glu Lys Met Leu Asp Ala Val Ile Asp Gly Thr
 645 650 655
 Pro Cys Phe Glu Gly Gly Asn Ser Arg Asn Val Cys Ile Asn Gly Ile
 660 665 670
 Cys Lys Met Val Gly Cys Asp Tyr Glu Ile Asp Ser Asn Ala Thr Glu
 675 680 685
 Asp Arg Cys Gly Val Cys Leu Gly Asp Gly Ser Ser Cys Gln Thr Val
 690 695 700
 Arg Lys Met Phe Lys Gln Lys Glu Gly Ser Gly Tyr Val Asp Ile Gly
 705 710 715 720
 Leu Ile Pro Lys Gly Ala Arg Asp Ile Arg Val Met Glu Ile Glu Gly
 725 730 735

Cura 468 SEQ list 0705

Ala Gly Asn Phe Leu Ala Ile Arg Ser Glu Asp Pro Glu Lys Tyr Tyr
740 745 750

Leu Asn Gly Gly Phe Ile Ile Gln Trp Asn Gly Asn Tyr Lys Leu Ala
755 760 765

Gly Thr Val Phe Gln Tyr Asp Arg Lys Gly Asp Leu Glu Lys Leu Met
770 775 780

Ala Thr Gly Pro Thr Asn Glu Ser Val Trp Ile Gln Leu Leu Phe Gln
785 790 795 800

Val Thr Asn Pro Gly Ile Lys Tyr Glu Tyr Thr Ile Gln Lys Asp Gly
805 810 815

Leu Asp Asn Asp Val Glu Gln Met Tyr Phe Trp Gln Tyr Gly His Trp
820 825 830

Thr Glu Cys Ser Val Thr Cys Gly Thr Gly Ile Arg Arg Gln Thr Ala
835 840 845

His Cys Ile Lys Lys Gly Arg Gly Met Val Lys Ala Thr Phe Cys Asp
850 855 860

Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala
865 870 875 880

Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr
885 890 895

Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr
900 905 910

Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu
915 920 925

Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro
930 935 940

Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly
945 950 955 960

Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu
965 970 975

Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu
980 985 990

Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr
995 1000 1005

Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro
1010 1015 1020

Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met
1025 1030 1035 1040

Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser
1045 1050 1055

Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln
1060 1065 1070

Cura 468 SEQ list 0705

Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser Thr Gly Ser Thr Ser Gln
1075 1080 1085

Pro Ile Leu Thr Ser Gln Ser Leu Ser Ile Gln Pro Ser Glu Glu Asn
1090 1095 1100

Val Ser Ser Ser Asp Thr Gly Pro Thr Ser Glu Gly Gly Leu Val Ala
1105 1110 1115 1120

Thr Thr Thr Ser Gly Ser Gly Leu Ser Ser Ser Arg Asn Pro Ile Thr
1125 1130 1135

Trp Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met
1140 1145 1150

Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys
1155 1160 1165

Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn
1170 1175 1180

Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr
1185 1190 1195 1200

Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met
1205 1210 1215

Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr
1220 1225 1230

Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu
1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn
1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser
1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly
1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly
1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys
1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp
1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His
1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser
1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp
1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala
1395 1400 1405

Cura 468 SEQ list 0705

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu
1410 1415 1420
Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly
1425 1430 1435 1440
Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp
1445 1450 1455
Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys
1460 1465 1470
His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly
1475 1480 1485
Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys
1490 1495 1500
Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro
1505 1510 1515 1520
Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu
1525 1530 1535
Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys
1540 1545 1550
Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe
1555 1560 1565
Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln
1570 1575 1580
Arg Leu Leu Gln Lys Ser Lys Glu Leu
1585 1590

<210> 31
<211> 1077
<212> PRT
<213> Homo sapiens

<400> 31

Arg Ser Gln Asp Glu Phe Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala
1 5 10 15
Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro
20 25 30
Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser
35 40 45
Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn
50 55 60
Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr
65 70 75 80
Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys
85 90 95
Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala

100

Page 44

445

Cura 468 SEQ list 0705

770		775		780
Leu 785	Arg	Tyr	Arg	Phe
				Asn 790
				Ala
				Pro
				Ile
				Ala
				Arg 795
				Asp
				Ser
				Leu
				Pro
				Pro 800
Tyr	Ser	Trp	His	Tyr 805
				Ala
				Pro
				Trp
				Thr
				Lys 810
				Cys
				Ser
				Ala
				Gln
				Cys 815
Gly	Gly	Ser	Gln 820	Val
				Gln
				Ala
				Val
				Glu 825
				Cys
				Arg
				Asn
				Gln
				Leu 830
				Asp
				Ser
Ser	Ala	Val 835	Ala	Pro
				His
				Tyr
				Cys 840
				Ser
				Ala
				His
				Ser
				Lys 845
				Leu
				Pro
				Lys
Arg	Gln 850	Arg	Ala	Cys
				Asn
				Thr 855
				Glu
				Pro
				Cys
				Pro
				Pro 860
				Asp
				Trp
				Val
				Val
Gly 865	Asn	Trp	Ser	Leu
				Cys 870
				Ser
				Arg
				Ser
				Cys
				Asp 875
				Ala
				Gly
				Val
				Arg
				Ser 880
Arg	Ser	Val	Val	Cys 885
				Gln
				Arg
				Arg
				Val
				Ser 890
				Ala
				Ala
				Glu
				Glu
				Lys 895
				Ala
Leu	Asp	Asp	Ser 900	Ala
				Cys
				Pro
				Gln
				Pro 905
				Arg
				Pro
				Pro
				Val
				Leu 910
				Glu
				Ala
Cys	His	Gly 915	Pro	Thr
				Cys
				Pro
				Pro 920
				Glu
				Trp
				Ala
				Ala
				Leu 925
				Asp
				Trp
				Ser
Glu	Cys 930	Thr	Pro	Ser
				Cys
				Gly 935
				Pro
				Gly
				Leu
				Arg
				His 940
				Arg
				Val
				Val
				Leu
Cys 945	Lys	Ser	Ala	Asp
				His 950
				Arg
				Ala
				Thr
				Leu
				Pro 955
				Pro
				Ala
				His
				Cys
				Ser 960
Pro	Ala	Ala	Lys	Pro
				Pro 965
				Ala
				Thr
				Met
				Arg 970
				Cys
				Asn
				Leu
				Arg
				Arg 975
				Cys
Pro	Pro	Ala	Arg 980	Trp
				Val
				Ala
				Gly
				Glu 985
				Trp
				Gly
				Glu
				Cys
				Ser 990
				Ala
				Gln
Cys	Gly	Val 995	Gly	Gln
				Arg
				Gln
				Arg
				Ser
				Val
				Arg
				Cys
				Thr 1005
				Ser
				His
				Thr
Gly	Gln 1010	Ala	Ser	His
				Glu
				Cys
				Thr 1015
				Glu
				Ala
				Leu
				Arg 1020
				Pro
				Pro
				Thr
				Thr
Gln	Gln	Cys	Glu	Ala
				Lys
				Cys
				Asp
				Ser
				Pro
				Thr 1035
				Pro
				Gly
				Asp
				Gly
				Pro 1040
Glu	Glu	Cys	Lys	Asp
				Val
				Asn
				Lys
				Val
				Ala
				Tyr
				Cys
				Pro
				Leu
				Val 1055
				Leu
Lys	Phe	Gln	Phe	Cys
				Ser
				Arg
				Ala
				Tyr
				Phe
				Arg
				Gln
				Met
				Cys
				Cys
				Lys
Thr	Cys	Gln	Gly	His
				1075

<210> 32
 <211> 997
 <212> PRT

Cura 468 SEQ list 0705

<213> Homo sapiens

<400> 32

Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro
 1 5 10 15
 Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala
 20 25 30
 Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro
 35 40 45
 Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro
 50 55 60
 Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala
 65 70 75 80
 Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr
 85 90 95
 Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg
 100 105 110
 Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys
 115 120 125
 His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala
 130 135 140
 Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn
 145 150 155 160
 Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly
 165 170 175
 His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu
 180 185 190
 Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val
 195 200 205
 Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln
 210 215 220
 Trp Arg Arg Pro Arg Leu Arg Arg Leu His Gln Arg Ser Val Ser Lys
 225 230 235 240
 Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys Met Val Glu
 245 250 255
 Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr Ile Met Asn
 260 265 270
 Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn Pro Ile His
 275 280 285
 Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu Glu Asp Leu
 290 295 300
 Lys Ile Thr His His Ala Asp Asn Thr Leu Lys Ser Phe Cys Lys Trp
 305 310 315 320

Cura 468 SEQ list 0705

Gln Lys Ser Ile Asn Met Lys Gly Asp Ala His Pro Leu His His Asp
325 330 335

Thr Ala Ile Leu Leu Thr Arg Lys Asp Leu Cys Ala Ala Met Asn Arg
340 345 350

Pro Cys Glu Thr Leu Gly Leu Ser His Val Ala Gly Met Cys Gln Pro
355 360 365

His Arg Ser Cys Ser Ile Asn Glu Asp Thr Gly Leu Pro Leu Ala Phe
370 375 380

Thr Val Ala His Glu Leu Gly His Ser Phe Gly Ile Gln His Asp Gly
385 390 395 400

Ser Gly Asn Asp Cys Glu Pro Val Gly Lys Arg Pro Phe Ile Met Ser
405 410 415

Pro Gln Leu Leu Tyr Asp Ala Ala Pro Leu Thr Trp Ser Arg Cys Ser
420 425 430

Arg Gln Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp Gly Leu Cys Leu
435 440 445

Asp Asp Pro Pro Ala Lys Asp Ile Ile Asp Phe Pro Ser Val Pro Pro
450 455 460

Gly Val Leu Tyr Asp Val Ser His Gln Cys Arg Leu Gln Tyr Gly Ala
465 470 475 480

Tyr Ser Ala Phe Cys Glu Asp Met Asp Asn Val Cys His Thr Leu Trp
485 490 495

Cys Ser Val Gly Thr Thr Cys His Ser Lys Leu Asp Ala Ala Val Asp
500 505 510

Gly Thr Arg Cys Gly Glu Asn Lys Trp Cys Leu Ser Gly Glu Cys Val
515 520 525

Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp Ser Gly Trp
530 535 540

Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly Val Gln Ser
545 550 555 560

Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys Gly Arg Tyr
565 570 575

Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu Gln Ala Cys
580 585 590

Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser His Phe Asp
595 600 605

Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn
610 615 620

Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe
625 630 635 640

Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln
645 650 655

Cura 468 SEQ list 0705

Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val
660 665 670

Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly
675 680 685

Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe
690 695 700

Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala
705 710 715 720

Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe
725 730 735

Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly
740 745 750

Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe
755 760 765

Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro
770 775 780

Thr Lys Glu Pro Val Trp Ile Gln Val Pro Ala Ser Arg Gly Pro Gly
785 790 795 800

Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr Leu His Gly Arg
805 810 815

Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr Glu Pro Gly Ser
820 825 830

Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val Ser Pro Ser Leu
835 840 845

Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly Gly Trp Gly Gln
850 855 860

Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu Val Leu Met Gly
865 870 875 880

Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser Asn Pro Gly Val
885 890 895

His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp Glu Val
900 905 910

Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys Cys Thr
915 920 925

Val Thr Cys Gly Arg Gly Glu Lys Trp Gly Arg His Ser Pro Thr Cys
930 935 940

Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His
945 950 955 960

Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe
965 970 975

Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala
980 985 990

Cura 468 SEQ list 0705

Gly Arg Val His Gly
995

<210> 33
<211> 854
<212> PRT
<213> Homo sapiens

<400> 33

Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu
1 5 10 15
Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly
20 25 30
Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp
35 40 45
Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser
50 55 60
Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn
65 70 75 80
Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile
85 90 95
Thr Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu
100 105 110
Gly Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser
115 120 125
Val Asn Glu Asp Ile Gly Leu Ala Thr Ala Phe Thr Ile Ala His Glu
130 135 140
Ile Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys
145 150 155 160
Gly Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr
165 170 175
Met Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Ser Arg Asp Tyr Ile
180 185 190
Thr Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro
195 200 205
Pro Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr
210 215 220
Asp Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln
225 230 235 240
Cys Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser
245 250 255
Asn Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys
260 265 270
Gln Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val
275 280 285

Cura 468 SEQ list 0705

Pro Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp
 290 295 300
 Thr Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser
 305 310 315 320
 Ser Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr
 325 330 335
 Cys Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys
 340 345 350
 Pro Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp
 355 360 365
 Ser Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly
 370 375 380
 Gly Gly Val Lys Ala Cys Ser Leu Thr Cys Leu Ala Glu Gly Phe Asn
 385 390 395 400
 Phe Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg
 405 410 415
 Pro Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly
 420 425 430
 Cys Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val
 435 440 445
 Cys Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser
 450 455 460
 Pro Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys
 465 470 475 480
 Gly Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His
 485 490 495
 Leu Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro
 500 505 510
 Gly Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln
 515 520 525
 Leu Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro
 530 535 540
 Ile Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro
 545 550 555 560
 Ala Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro
 565 570 575
 Pro Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys
 580 585 590
 Ala Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp
 595 600 605
 Ser Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro
 610 615 620

Cura 468 SEQ list 0705

Lys Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val
 625 630 635 640
 Val Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg
 645 650 655
 Ser Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys
 660 665 670
 Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu
 675 680 685
 Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp
 690 695 700
 Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val
 705 710 715 720
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys
 725 730 735
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg
 740 745 750
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala
 755 760 765
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His
 770 775 780
 Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr
 785 790 795 800
 Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly
 805 810 815
 Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val
 820 825 830
 Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys
 835 840 845
 Lys Thr Cys His Gly His
 850

<210> 34

<211> 860

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (450)

<223> wherein Xaa is any amino acid.

<400> 34

Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
 1 5 10 15

Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
 20 25 30

Cura 468 SEQ list 0705

Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
 35 40 45
 Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
 50 55 60
 Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
 65 70 75 80
 Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
 85 90 95
 His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
 100 105 110
 Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
 115 120 125
 Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
 130 135 140
 Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
 145 150 155 160
 Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
 165 170 175
 Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
 180 185 190
 Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
 195 200 205
 Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
 210 215 220
 Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
 225 230 235 240
 Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
 245 250 255
 Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
 260 265 270
 His Tyr Ile Leu Ser Val Met Asn Ile Val Ala Lys Leu Tyr Arg Asp
 275 280 285
 Ser Ser Leu Gly Asn Val Val Asn Ile Ile Val Ala Arg Leu Ile Val
 290 295 300
 Leu Thr Glu Asp Gln Pro Asn Leu Glu Ile Asn His His Ala Asp Lys
 305 310 315 320
 Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser Ile Leu Ser His Gln
 325 330 335
 Ser Asp Gly Asn Thr Ile Pro Glu Asn Gly Ile Ala His His Asp Asn
 340 345 350
 Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Thr Tyr Lys Asn Lys Pro
 355 360 365

Cura 468 SEQ list 0705

Cys Gly Thr Leu Gly Leu Ala Ser Val Ala Gly Met Cys Glu Pro Glu
 370 375 380
 Arg Ser Cys Ser Ile Asn Glu Asp Ile Gly Leu Gly Ser Ala Phe Thr
 385 390 395 400
 Ile Ala His Glu Ile Val His Asn Phe Gly Met Asn His Asp Gly Ile
 405 410 415
 Gly Asn Ser Cys Gly Arg Lys Val Met Lys Gln Gln Asn Tyr Gly Ser
 420 425 430
 Ser His Tyr Cys Glu Tyr Gln Ser Phe Phe Leu Val Cys Leu Gln Ser
 435 440 445
 Arg Xaa His His Gln Leu Phe Arg Glu Val Cys Arg Glu Leu Trp Cys
 450 455 460
 Leu Ser Lys Ser Asn Arg Cys Val Thr Asn Ser Ile Pro Ala Ala Glu
 465 470 475 480
 Gly Thr Leu Cys Gln Thr Gly Asn Ile Glu Lys Gly Trp Cys Tyr Gln
 485 490 495
 Gly Asp Cys Val Pro Phe Gly Thr Trp Pro Gln Ser Ile Asp Gly Gly
 500 505 510
 Trp Gly Pro Trp Ser Leu Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
 515 520 525
 Gly Val Ser Ser Ser Leu Arg His Cys Asp Ser Pro Ala Pro Ser Gly
 530 535 540
 Gly Gly Lys Tyr Cys Leu Gly Glu Arg Lys Arg Tyr Arg Ser Cys Asn
 545 550 555 560
 Thr Asp Pro Cys Pro Leu Gly Ser Arg Asp Phe Arg Glu Lys Gln Cys
 565 570 575
 Ala Asp Phe Asp Asn Met Pro Phe Arg Gly Lys Tyr Tyr Asn Trp Lys
 580 585 590
 Pro Tyr Thr Gly Gly Gly Val Lys Pro Cys Ala Leu Asn Cys Leu Ala
 595 600 605
 Glu Gly Tyr Asn Phe Tyr Thr Glu Arg Ala Pro Ala Val Ile Asp Gly
 610 615 620
 Thr Gln Cys Asn Ala Asp Ser Leu Asp Ile Cys Ile Asn Gly Glu Cys
 625 630 635 640
 Lys His Val Gly Cys Asp Asn Ile Leu Gly Ser Asp Ala Arg Glu Asp
 645 650 655
 Arg Cys Arg Val Cys Gly Gly Gly Gly Ser Thr Cys Asp Ala Ile Glu
 660 665 670
 Gly Phe Phe Asn Asp Ser Leu Pro Arg Gly Gly Tyr Met Glu Val Val
 675 680 685
 Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met
 690 695 700

Cura 468 SEQ list 0705

Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile
705 710 715 720
Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly
725 730 735
Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu
740 745 750
Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln
755 760 765
Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg
770 775 780
Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro
785 790 795 800
Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg
805 810 815
Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr
820 825 830
Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe
835 840 845
Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu
850 855 860

<210> 35
<211> 936
<212> PRT
<213> Homo sapiens

<400> 35
Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
1 5 10 15
Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
20 25 30
Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
35 40 45
Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
50 55 60
Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
65 70 75 80
Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
85 90 95
Asn Asp Gln Asp Asn Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
100 105 110
Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
115 120 125
Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys

Cura 468 SEQ list 0705

130		135		140												
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His	
145					150					155					160	
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly	
				165					170					175		
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr	
			180					185					190			
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	
		195					200					205				
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	
	210					215					220					
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	
225					230					235					240	
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	
				245					250					255		
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	
			260					265					270			
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	
		275					280					285				
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	
	290					295					300					
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	
305					310				315						320	
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	
				325				330						335		
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	
			340					345					350			
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	
		355					360					365				
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	
	370					375					380					
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	
385					390					395					400	
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	
				405					410					415		
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	
			420					425					430			
Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	
		435					440					445				
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser	
	450					455					460					
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	

Cura 468 SEQ list 0705
475

465					470											480
Lys	His	Tyr	Asp	Gly 485	Ser	Tyr	Ser	Thr	Phe 490	Gly	Glu	Arg	Tyr	Gly 495	Arg	
Asn	Gln	Gly	Asn 500	Thr	Trp	Leu	Thr	Ala 505	Phe	Val	Leu	Lys	Thr 510	Phe	Ala	
Gln	Ala	Arg 515	Ala	Tyr	Ile	Phe	Ile 520	Asp	Glu	Ala	His	Ile 525	Thr	Gln	Ala	
Leu	Ile 530	Trp	Leu	Ser	Gln	Arg 535	Gln	Lys	Asp	Asn	Gly 540	Cys	Phe	Arg	Ser	
Ser 545	Gly	Ser	Leu	Leu	Asn 550	Asn	Ala	Ile	Lys	Gly 555	Gly	Val	Glu	Asp	Glu 560	
Val	Thr	Leu	Ser	Ala 565	Tyr	Ile	Thr	Ile	Ala 570	Leu	Leu	Glu	Ile	Pro 575	Leu	
Thr	Val	Thr	His 580	Pro	Val	Val	Arg	Asn 585	Ala	Leu	Phe	Cys	Leu 590	Glu	Ser	
Ala	Trp	Lys 595	Thr	Ala	Gln	Glu	Gly 600	Asp	His	Gly	Ser	His 605	Val	Tyr	Thr	
Lys	Ala 610	Leu	Leu	Ala	Tyr	Ala 615	Phe	Ala	Leu	Ala	Gly 620	Asn	Gln	Asp	Lys	
Arg 625	Lys	Glu	Val	Leu	Lys 630	Ser	Leu	Asn	Glu	Glu 635	Ala	Val	Lys	Lys	Asp 640	
Asn	Ser	Val	His	Trp 645	Glu	Arg	Pro	Gln	Lys 650	Pro	Lys	Ala	Pro	Val 655	Gly	
His	Phe	Tyr	Glu 660	Pro	Gln	Ala	Pro	Ser 665	Ala	Glu	Val	Glu 670	Met	Thr	Ser	
Tyr	Val	Leu 675	Leu	Ala	Tyr	Leu	Thr 680	Ala	Gln	Pro	Ala	Pro 685	Thr	Ser	Glu	
Asp	Leu 690	Thr	Ser	Ala	Thr	Asn 695	Ile	Val	Lys	Trp	Ile 700	Thr	Lys	Gln	Gln	
Asn 705	Ala	Gln	Gly	Gly	Phe 710	Ser	Ser	Thr	Gln	Asp 715	Thr	Val	Val	Ala	Leu 720	
His	Ala	Leu	Ser	Lys 725	Tyr	Gly	Ala	Ala	Thr 730	Phe	Thr	Arg	Thr	Gly 735	Lys	
Ala	Ala	Gln	Val 740	Thr	Ile	Gln	Ser	Ser 745	Gly	Thr	Phe	Ser	Ser 750	Lys	Phe	
Gln	Val	Asp 755	Asn	Asn	Asn	Arg	Leu 760	Leu	Leu	Gln	Gln	Val 765	Ser	Leu	Pro	
Glu	Leu 770	Pro	Gly	Glu	Tyr	Ser 775	Met	Lys	Val	Thr	Gly 780	Glu	Gly	Cys	Val	
Tyr 785	Leu	Gln	Thr	Ser	Leu 790	Lys	Tyr	Asn	Ile	Leu 795	Pro	Glu	Lys	Glu	Glu 800	
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	

Cura 468 SEQ list 0705

805 810 815

Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr
820 825 830

Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val
835 840 845

Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser
850 855 860

Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr
865 870 875 880

Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu
885 890 895

Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
900 905 910

Asp Tyr Tyr Glu Thr Gly Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
915 920 925

Cys Ser Lys Asp Leu Gly Asn Ala
930 935

<210> 36
<211> 898
<212> PRT
<213> Homo sapiens

<400> 36

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
1 5 10 15

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
20 25 30

Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
35 40 45

Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
50 55 60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
65 70 75 80

Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
85 90 95

Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
100 105 110

Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
115 120 125

Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
130 135 140

Ile Arg Lys Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro
145 150 155 160

Cura 468 SEQ list 0705

Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala
165 170 175

Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly
180 185 190

Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala
195 200 205

Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr
210 215 220

Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn
225 230 235 240

Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro
245 250 255

Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile
260 265 270

Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser
275 280 285

Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln
290 295 300

Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys
305 310 315 320

Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys
325 330 335

Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser
340 345 350

Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala
355 360 365

Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln
370 375 380

Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn
385 390 395 400

Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
405 410 415

Thr Gln Gln Leu Thr Pro Glu Val Lys Ser Lys Ala Ile Gly Tyr Leu
420 425 430

Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
435 440 445

Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
450 455 460

Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
465 470 475 480

Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
485 490 495

Cura 468 SEQ list 0705

Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
 500 505 510
 Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
 515 520 525
 Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
 530 535 540
 Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
 545 550 555 560
 Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
 565 570 575
 Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
 580 585 590
 Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
 595 600 605
 Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
 610 615 620
 Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
 625 630 635 640
 Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
 645 650 655
 Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe
 660 665 670
 Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
 675 680 685
 Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
 690 695 700
 Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
 705 710 715 720
 Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
 725 730 735
 Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
 740 745 750
 Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
 755 760 765
 Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
 770 775 780
 Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
 785 790 795 800
 Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
 805 810 815
 Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
 820 825 830

Cura 468 SEQ list 0705

Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
835 840 845
Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
850 855 860
Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp
865 870 875 880
Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
885 890 895

Asn Ala

<210> 37
<211> 936
<212> PRT
<213> Homo sapiens

<400> 37

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
1 5 10 15
Ser Ala Lys Tyr Asp Val Glu Asn Glu Leu Ala Asn Lys Val Asp Leu
20 25 30
Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
35 40 45
Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
50 55 60
Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
65 70 75 80
Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
85 90 95
Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
100 105 110
Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
115 120 125
Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
130 135 140
Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
145 150 155 160
Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly
165 170 175
Arg Gly His Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr
180 185 190
Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val
195 200 205
Asn Ser Ala Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile
210 215 220

Cura 468 SEQ list 0705

Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu
 225 230 235 240
 Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val
 245 250 255
 Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu
 260 265 270
 Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val
 275 280 285
 Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu
 290 295 300
 Gln Ala Pro His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp
 305 310 315 320
 Ala Val Thr Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala
 325 330 335
 Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val
 340 345 350
 Pro Glu His Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu
 355 360 365
 Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro
 370 375 380
 Ser Gly Gly Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn
 385 390 395 400
 Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile
 405 410 415
 Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr
 420 425 430
 Gly Cys Gly Glu Glx Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val
 435 440 445
 Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser
 450 455 460
 Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr
 465 470 475 480
 Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg
 485 490 495
 Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala
 500 505 510
 Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala
 515 520 525
 Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser
 530 535 540
 Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu
 545 550 555 560

Cura 468 SEQ list 0705

Val	Thr	Leu	Ser	Ala 565	Tyr	Ile	Lys	Ile	Ala 570	Leu	Leu	Glu	Ile	Pro 575	Leu	
Thr	Val	Thr	His 580	Pro	Val	Val	Arg	Asn 585	Ala	Leu	Phe	Cys	Leu 590	Glu	Ser	
Ala	Trp	Lys 595	Thr	Ala	Glu	Glu	Gly 600	Asp	His	Gly	Ser	His 605	Val	Tyr	Thr	
Lys	Ala 610	Leu	Leu	Ala	Tyr	Ala 615	Phe	Ala	Leu	Ala	Gly 620	Asn	Gln	Asp	Lys	
Arg 625	Lys	Glu	Val	Leu	Lys 630	Ser	Leu	Asn	Glu	Glu 635	Ala	Val	Lys	Lys	Asp 640	
Asn	Ser	Val	His	Trp 645	Glu	Arg	Pro	Gln	Lys 650	Pro	Lys	Ala	Pro	Val 655	Gly	
His	Phe	Tyr	Glu 660	Pro	Gln	Ala	Pro	Ser 665	Ala	Glu	Val	Glu	Met 670	Thr	Ser	
Tyr	Val	Leu 675	Leu	Ala	Tyr	Leu	Thr 680	Ala	Gln	Pro	Ala	Pro 685	Thr	Ser	Glu	
Asp 690	Leu	Thr	Ser	Ala	Thr	Asn 695	Ile	Val	Lys	Trp	Ile 700	Thr	Lys	Gln	Gln	
Asn 705	Ala	Gln	Gly	Gly	Phe 710	Ser	Ser	Thr	Gln	Asp 715	Lys	Val	Val	Ala	Leu 720	
His	Ala	Leu	Ser	Lys 725	Tyr	Gly	Ala	Ala	Thr 730	Phe	Thr	Arg	Thr	Gly 735	Lys	
Ala	Ala	Gln	Val 740	Thr	Ile	Gln	Ser	Ser 745	Gly	Thr	Phe	Ser	Ser 750	Lys	Phe	
Gln	Val	Asp 755	Asn	Asn	Asn	Arg	Leu 760	Leu	Leu	Gln	Gln	Val 765	Ser	Leu	Pro	
Glu 770	Leu	Pro	Gly	Glu	Tyr	Ser 775	Met	Lys	Val	Thr	Gly 780	Glu	Gly	Cys	Val	
Tyr 785	Leu	Gln	Thr	Ser	Leu 790	Lys	Tyr	Asn	Ile	Leu 795	Pro	Glu	Lys	Glu	Glu 800	
Phe	Pro	Phe	Ala	Leu 805	Gly	Val	Gln	Thr	Leu 810	Pro	Gln	Thr	Cys	Asp 815	Glu	
Pro	Lys	Ala	His 820	Thr	Ser	Phe	Gln	Ile 825	Ser	Leu	Ser	Val	Ser 830	Tyr	Thr	
Gly	Ser	Arg 835	Ser	Ala	Ser	Asn	Met 840	Ala	Ile	Val	Asp	Val 845	Lys	Met	Val	
Ser	Gly 850	Phe	Ile	Pro	Leu	Lys 855	Pro	Thr	Val	Lys	Met 860	Leu	Glu	Arg	Ser	
Asn 865	His	Val	Ser	Arg	Thr 870	Glu	Val	Ser	Ser	Asn 875	His	Val	Leu	Ile	Tyr 880	
Leu	Asp	Lys	Val	Ser 885	Asn	Gln	Thr	Leu	Ser 890	Leu	Phe	Phe	Thr	Val 895	Leu	

Cura 468 SEQ list 0705

Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
 900 905 910
 Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
 915 920 925
 Cys Ser Lys Asp Leu Gly Asn Ala
 930 935

<210> 38
 <211> 931
 <212> PRT
 <213> Rattus norvegicus

<400> 38
 Arg Leu Val Leu Tyr Ala Ile Leu Pro Asn Gly Glu Val Val Gly Asp
 1 5 10 15
 Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Val Phe Arg Pro Asn Ser Gly Leu Pro Ala Thr Arg Ala Leu Leu Ser
 35 40 45
 Val Met Ala Ser Pro Gln Ser Leu Cys Gly Leu Arg Ala Val Asp Gln
 50 55 60
 Ser Val Leu Leu Met Lys Pro Glu Thr Glu Leu Ser Ala Ser Leu Ile
 65 70 75 80
 Tyr Asp Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gln Gly Ala
 85 90 95
 Asp Gln Arg Glu Glu Asp Thr Asn Gly Cys Val Lys Gln Asn Asp Thr
 100 105 110
 Tyr Ile Asn Gly Ile Leu Tyr Ser Pro Val Gln Asn Thr Asn Glu Glu
 115 120 125
 Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn
 130 135 140
 Ser Asn Ile Arg Lys Pro Lys Val Cys Glu Arg Leu Arg Asp Asn Lys
 145 150 155 160
 Gly Ile Pro Ala Ala Tyr His Leu Val Ser Gln Ser His Met Asp Ala
 165 170 175
 Phe Leu Glu Ser Ser Glu Ser Pro Thr Glu Thr Arg Arg Ser Tyr Phe
 180 185 190
 Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asp Ser Ala Gly Val
 195 200 205
 Ala Glu Val Glu Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala
 210 215 220
 Gly Ala Phe Cys Leu Ser Asn Asp Thr Gly Leu Gly Leu Ser Pro Val
 225 230 235 240
 Val Gln Phe Gln Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro

255

Cura 468 SEQ list 0705
585 590

580
Arg Gly Gly Ala Gly Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala
595 600 605
Tyr Ala Phe Ala Leu Ala Gly Pro Val Val Arg Asn Ala Leu Phe Cys
610 615 620
Leu Asp Thr Ala Trp Lys Ser Ala Arg Gly Gly Ala Gly Gly Ser His
625 630 635 640
Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Pro
645 650 655
Gln Ala Thr Ser Ala Glu Val Glu Met Thr Ala Tyr Val Leu Leu Ala
660 665 670
Tyr Leu Thr Thr Glu Pro Ala Pro Thr Gln Glu Asp Leu Thr Ala Ala
675 680 685
Met Leu Ile Val Lys Trp Leu Thr Lys Gln Gln Asn Ser His Gly Gly
690 695 700
Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys
705 710 715 720
Tyr Gly Ser Ala Thr Phe Thr Arg Ala Lys Lys Ala Ala Gln Val Thr
725 730 735
Ile Arg Ser Ser Gly Thr Phe Ser Thr Lys Phe Gln Val Asn Asn Asn
740 745 750
Asn Gln Leu Leu Leu Gln Arg Val Thr Leu Pro Thr Val Pro Gly Asp
755 760 765
Tyr Thr Val Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser
770 775 780
Leu Lys Tyr Ser Val Leu Pro Arg Glu Glu Glu Phe Pro Phe Ala Val
785 790 795 800
Val Val Gln Thr Leu Pro Gly Thr Cys Glu Asp Pro Lys Ala His Thr
805 810 815
Ser Phe Gln Ile Ser Leu Asn Ile Ser Tyr Thr Gly Ser Arg Ser Glu
820 825 830
Ser Asn Met Ala Ile Ala Asp Val Lys Met Val Ser Gly Phe Ile Pro
835 840 845
Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Val His Val Ser Arg
850 855 860
Thr Glu Val Ser Asn Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser
865 870 875 880
Asn Gln Thr Val Asn Leu Ser Phe Thr Val Gln Gln Asp Ile Pro Ile
885 890 895
Arg Asp Leu Lys Pro Ala Val Val Lys Val Tyr Asp Tyr Tyr Glu Lys
900 905 910
Asp Glu Phe Ala Val Ala Lys Tyr Ser Ala Pro Cys Ser Thr Asp Tyr

915

920

925

Gly Asn Ala
930

<210> 39
<211> 941
<212> PRT
<213> *Cavia porcellus*

<400> 39

Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp
1 5 10 15
Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu
20 25 30
Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg
35 40 45
Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln
50 55 60
Ser Val Leu Leu Arg Lys Pro Glu Ala Val Leu Ser Ala Ser Ser Val
65 70 75 80
Tyr Ala Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gly Leu Leu
85 90 95
Gly Gln Gln Glu Glu Asn Asp Gly Glu Cys Val Ser Leu Tyr Asn Thr
100 105 110
Tyr Ile Asp Gly Ile Leu Tyr Ser Pro Glu Pro Asn Ile Asn Glu Lys
115 120 125
Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn
130 135 140
Thr Lys Ile Gln Lys Pro Gln Leu Cys Ala His Val Gln Lys Phe Glu
145 150 155 160
Val Pro Thr Met Ala Tyr Ser Tyr Ser Glu Ser Ser Ser Phe Arg Ser
165 170 175
Gly Pro Arg Arg Val Pro Ala Val Gly Ile Ala Ala Thr Tyr Ser Glu
180 185 190
Pro Pro Lys Glu Thr Val Arg Thr Tyr Ser Pro Glu Thr Trp Ile Trp
195 200 205
Asp Leu Lys Val Thr Asp Ser Ser Gly Val Ala Glu Val Glu Val Thr
210 215 220
Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser
225 230 235 240
Asn Asp Thr Gly Leu Gly Leu Ser Pro Thr Ala Ser Leu Arg Ala Phe
245 250 255
Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly
260 265 270

Cura 468 SEQ list 0705

Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn Tyr Leu Pro Asp Cys
275 280 285

Ile Arg Ile Ser Val His Leu Glu Ala Ser Pro Lys Phe Leu Ala Glu
290 295 300

Pro Lys Ala Lys Glu Gln Glu Ser Tyr Cys Val Cys Gly Asn Glu Arg
305 310 315 320

Gln Thr Val Ser Trp Val Val Thr Pro Lys Ser Leu Gly Asn Val Asn
325 330 335

Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Ser Glu Leu Cys Gly Asn
340 345 350

Glu Lys Thr Val Val Pro Thr Tyr Gly Lys Lys Asp Thr Ile Ile Lys
355 360 365

Pro Leu Leu Val Glu Pro Glu Gly Ile Glu Lys Glu Glu Thr Trp Thr
370 375 380

Ser Leu Ile Arg Val Ser Asp Thr Thr Val Ser Glu Lys Leu His Leu
385 390 395 400

Glu Leu Pro Ser Asn Val Ile Gln Asp Ser Ala Arg Ala Thr Val Ser
405 410 415

Ile Leu Gly Asp Ile Leu Gly Ser Ala Met Gln Asn Ile Gln Asn Leu
420 425 430

Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Val Leu Phe Ala
435 440 445

Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr
450 455 460

Pro Asp Ile Lys Ser Lys Ala Ile Ser Tyr Leu Ser Thr Gly Tyr Gln
465 470 475 480

Arg Gln Leu Asn Tyr Lys His Arg Asp Gly Ser Tyr Ser Thr Phe Gly
485 490 495

Glu Asn Tyr Arg Gly Gly Gln Gly Asn Thr Trp Leu Thr Ala Phe Val
500 505 510

Leu Lys Thr Phe Ser Gln Ala Arg Lys Tyr Ile Phe Ile Asp Glu Ala
515 520 525

His Ile Thr Gln Ala Leu Ser Trp Leu Ser Gln Lys Gln Lys Asp Asn
530 535 540

Gly Cys Phe Trp Ser Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly
545 550 555 560

Gly Val Glu Asp Glu Ile Ser Leu Ser Ala Tyr Ile Thr Ile Ala Leu
565 570 575

Leu Glu Met Ser Leu Pro Asp Thr His Pro Val Val Arg Asn Ala Leu
580 585 590

Phe Cys Leu Glu Ser Ala Trp Lys Ser Ala Lys Glu Gly Thr His Gly
595 600 605

Cura 468 SEQ list 0705

Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala
610 615 620

Gly Asn Gln Glu Arg Lys Lys Glu Ile Leu Lys Ser Leu Glu Asp Glu
625 630 635 640

Gly Val Lys Glu Asp Asn Ser Leu His Trp Ala Arg Pro Gln Lys Pro
645 650 655

Lys Val Ser Glu Gly Phe Leu Phe Lys Ser Gln Ala Pro Ser Ala Glu
660 665 670

Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr Leu Thr Ala Arg Pro
675 680 685

Ala Pro Thr Pro Glu Asp Leu Thr Ser Ala Thr Asp Ile Val Asn Trp
690 695 700

Val Thr Lys Gln Gln Asn Ser His Gly Gly Tyr Ser Ser Thr Gln Asp
705 710 715 720

Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr Ala Ala Ala Thr Phe
725 730 735

Thr Arg Thr Glu Lys Ala Ala Gln Val Thr Ile Lys Ser Ser Gly Thr
740 745 750

Phe Ser Thr Asn Phe Glu Val Asn His Asn Asn Arg Leu Leu Leu Gln
755 760 765

Gln Val Ser Leu Pro Thr Val Ser Asp Ser Tyr Thr Ile Thr Val Thr
770 775 780

Gly Glu Gly Asn Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Val Pro
785 790 795 800

Ser Glu Lys Gly Thr Phe Pro Phe Ala Leu Glu Ala Glu Thr Val Pro
805 810 815

Gln Ala Cys Asp Gly Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu
820 825 830

Asn Val Ser Tyr Ile Gly Ser Arg Pro Val Ser Asn Met Ala Ile Val
835 840 845

Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys
850 855 860

Asn Leu Glu Lys Ser Glu His Ile Ser Arg Thr Glu Val Ser Asn Asn
865 870 875 880

His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu
885 890 895

Ser Phe Phe Val Val Gln Asp Ile Glu Val Arg Asp Leu Lys Pro Ala
900 905 910

Ile Ile Lys Val Tyr Asp Tyr Tyr Glu Thr Asn Glu Phe Ala Ile Ala
915 920 925

Glu Tyr His Ala Pro Cys Ser Lys Asp Pro Gly Asn Ala
930 935 940

Cura 468 SEQ list 0705

<210> 40
 <211> 373
 <212> PRT
 <213> Mus musculus

<400> 40
 Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr
 1 5 10 15
 Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu
 20 25 30
 Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser
 35 40 45
 Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
 50 55 60
 Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
 65 70 75 80
 Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
 85 90 95
 Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
 100 105 110
 Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
 145 150 155 160
 Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
 165 170 175
 Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
 180 185 190
 Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val
 195 200 205
 Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
 210 215 220
 Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
 225 230 235 240
 Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
 245 250 255
 Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
 260 265 270
 Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
 275 280 285
 Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
 290 295 300

Cura 468 SEQ list 0705

Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
 305 310 315 320
 Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
 325 330 335
 Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
 340 345 350
 Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His
 355 360 365
 Ile Pro Ser Cys Glu
 370

<210> 41
 <211> 347
 <212> PRT
 <213> Oryzctolagus cuniculus

<400> 41
 Met Ser Asn Leu Thr Val Gly Cys Leu Ala Asn Ala Thr Val Cys Glu
 1 5 10 15
 Gly Ala Ser Cys Val Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser
 20 25 30
 Val Val Leu Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe
 35 40 45
 Ser Met Gly Cys Asn Val Glu Ile Lys Lys Phe Leu Gly His Ile Arg
 50 55 60
 Arg Pro Trp Gly Ile Phe Ile Gly Phe Leu Cys Gln Phe Gly Ile Met
 65 70 75 80
 Pro Leu Thr Gly Phe Val Leu Ala Val Ala Phe Gly Ile Met Pro Ile
 85 90 95
 Gln Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ala
 100 105 110
 Ser Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val
 115 120 125
 Ser Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu
 130 135 140
 Cys Leu Tyr Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val
 145 150 155 160
 Ile Pro Tyr Asp Asn Ile Gly Thr Ser Leu Val Ala Leu Val Val Pro
 165 170 175
 Val Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys
 180 185 190
 Ile Ile Leu Lys Val Gly Ser Ile Ala Gly Ala Val Leu Ile Val Leu
 195 200 205
 Ile Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu

Cura 468 SEQ list 0705

210 215 220
Pro Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Met Ala Gly Tyr Ser
225 230 235 240
Leu Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys
245 250 255
Arg Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser
260 265 270
Thr Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Thr Tyr Val Phe
275 280 285
Thr Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile
290 295 300
Phe Leu Gly Ile Tyr Val Ala Tyr Arg Lys Cys His Gly Lys Asn Asp
305 310 315 320
Ala Glu Phe Pro Asp Ile Lys Asp Thr Lys Thr Glu Pro Glu Ser Ser
325 330 335
Phe His Gln Met Asn Gly Gly Phe Gln Pro Glu
340 345

<210> 42
<211> 348
<212> PRT
<213> Rattus norvegicus

<400> 42
Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly
1 5 10 15
Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg
50 55 60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160

Cura 468 SEQ list 0705

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175
Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190
Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
195 200 205
Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
210 215 220
Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
225 230 235 240
Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255
Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285
Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile
290 295 300
Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala
305 310 315 320
Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe
325 330 335
Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 43
<211> 348
<212> PRT
<213> Mus musculus

<400> 43
Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
1 5 10 15
Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
50 55 60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110

Cura 468 SEQ list 0705

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140

Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175

Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190

Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
195 200 205

Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
210 215 220

Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
225 230 235 240

Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255

Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270

Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285

Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
290 295 300

Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
305 310 315 320

Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
325 330 335

Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 44
<211> 348
<212> PRT
<213> Mus musculus

<400> 44
Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
1 5 10 15

Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45

Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg

Cura 468 SEQ list 0705
60

50 55
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175
Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190
Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
195 200 205
Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
210 215 220
Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
225 230 235 240
Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255
Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285
Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
290 295 300
Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
305 310 315 320
Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
325 330 335
Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 45
<211> 348
<212> PRT
<213> Homo sapiens

<400> 45

Cura 468 SEQ list 0705

Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly
1 5 10 15
Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg
50 55 60
Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160
Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175
Ser Ile Gly Met Tyr Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
180 185 190
Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
195 200 205
Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Thr Ile Glu Pro
210 215 220
Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu
225 230 235 240
Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg
245 250 255
Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285
Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu
290 295 300
Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr
305 310 315 320
Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe
325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345 Cura 468 SEQ list 0705

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140
 Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
 195 200 205
 Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
 210 215 220
 Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
 225 230 235 240
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
 245 250 255
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
 260 265 270

Cura 468 SEQ list 0705

<210> 47
 <211> 272
 <212> PRT
 <213> Rattus norvegicus

<400> 47

```

Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1          5          10          15
Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
          20          25          30
Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
          35          40          45
Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
          50          55          60
Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65          70          75          80
Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
          85          90          95
Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu
          100          105          110
Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
          115          120          125
Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
          130          135          140
Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
145          150          155          160
Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
          165          170          175
Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
          180          185          190
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
          195          200          205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
          210          215          220
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
225          230          235          240
Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
          245          250          255
Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
          260          265          270
    
```

Cura 468 SEQ list 0705

<210> 48

<211> 1798

<212> PRT

<213> *Drosophila melanogaster*

<400> 48

```

Met Glu Met Arg Glu Val Leu Ser Arg Glu Gly Arg Glu Ala Lys Asn
 1          5          10          15
Leu Leu Val Tyr Gln Phe Cys Asp Glu Thr Thr Ser Ser Gly Ala Thr
          20          25          30
Ser Gly Phe Gly Ser Thr Gly Gly Asp Val Gly Gly Gly Ser Gly Gly
 35          40          45
Asp Gly Pro Ala Val Gly Ser Gly Gly Val Leu Leu Asn Gly Asp Cys
 50          55          60
Tyr Arg Lys Pro Pro Met Val Pro Pro Lys Ser Pro Asn Gly Thr Pro
 65          70          75          80
Lys Asn Cys Gln Ser Pro Thr Ser Pro Arg Leu Lys Ser Ser Ala Ser
          85          90          95
Val Gly Cys Gly Gly Gly Ser Ser Gly Gly Pro Arg Val Arg Ser Ala
          100          105          110
Ser Thr Gly Arg Asp Lys Lys Ser Glu Leu Gln Ala Arg Tyr Trp Ala
          115          120          125
Leu Leu Phe Gly Asn Leu Gln Arg Ala Ile Asn Glu Ile Tyr Gln Thr
          130          135          140
Val Glu Cys Tyr Glu Asn Ile Ser Ser Cys Gln Glu Thr Ile Leu Val
          145          150          155          160
Leu Glu Asn Tyr Val Arg Asp Phe Lys Ala Leu Cys Glu Trp Phe Lys
          165          170          175
Val Ser Trp Asp Tyr Glu Ser Arg Pro Leu Gln Gln Arg Pro Gln Ser
          180          185          190
Leu Ala Trp Glu Val Arg Lys Ser Asn Pro Thr Pro Arg Val Arg Thr
          195          200          205
Arg Ser Leu Cys Ser Pro Asn Asn Ser Gly Lys Ser Ser Pro Ala Leu
          210          215          220
Phe Pro Gly Thr Gln Ser Gly Glu Thr Ser Pro Phe Cys Asp Asn Gly
          225          230          235          240
Gln Ile Ser Pro Arg Lys Leu Leu Arg Ala Tyr Asp Gln Val Pro Lys
          245          250          255
Gly Ala Met Arg Leu Asn Val Arg Glu Leu Phe Ala Ala Ser Lys Arg
          260          265          270
Ala Thr Gln Gly Ser Ser Gln Ser Asp Asn Met Glu Gly Pro Leu Asp
          275          280          285
Leu Ser Gly Asp Lys Ser Asn Phe Val Leu Arg Ser Thr Gln Tyr Ala
          290          295          300

```

Cura 468 SEQ list 0705

Gln Thr Asp Leu Glu Asp Pro His Leu Thr Leu Ala Asp Val Arg Glu
305 310 315 320

Lys Met Arg Met Glu Ala Glu Glu Arg Glu Ala Gln Asn Arg Ile Glu
325 330 335

Asn Glu Ala Leu Glu Glu Val Thr Ile Pro Ile Asp Asn Glu Asp Ala
340 345 350

Thr Glu Ser Leu Asn Lys Gln Glu Pro Ser Ser Leu Glu Leu Pro Ile
355 360 365

His Asn Val Ala Asp Leu Ser Lys Glu Pro Glu Leu Met Glu Ala Ala
370 375 380

Ser Glu Ala Thr Ala Leu Glu Met Thr Val Ala Ser Leu Glu Ser Met
385 390 395 400

Glu Asn Ala Leu Leu Asn Gln Gln Ala Asn Lys Glu Pro Thr Pro Pro
405 410 415

Ser Thr Val Ile Lys Pro Leu Ala Glu Ile Leu Lys Lys Pro Gln Pro
420 425 430

Leu Asn Pro Leu Ser Gly Asn Asn Val Gln Asn Ser Pro Leu Lys Tyr
435 440 445

Ser Ser Val Leu Asn Arg Pro Ser Lys Lys Met Ile Pro Pro Pro Gly
450 455 460

Gly Val Ala Ala Gln Lys Thr Ile Ser Thr Lys Pro Gly Leu Val Lys
465 470 475 480

Pro Asn Leu Thr Thr Thr Val Asn Gly Leu Arg Ser Thr Lys Thr Ala
485 490 495

Thr Ala Pro Pro Ala Ile Lys Thr Thr Gly Arg Ser Gly Leu Gln Arg
500 505 510

His Pro Arg Pro Ser Ser Lys Thr Glu Cys Tyr Gly Pro Pro Asn Asn
515 520 525

Val Ala Ser Arg Leu Ser Ala Arg Ser Arg Thr Ile Asn Thr Leu Lys
530 535 540

Ala Glu Asn Gln His Ser Glu Pro Lys Gln Ile Gln Pro Pro Thr Asp
545 550 555 560

Ala Asp Asp Gly Trp Leu Thr Val Lys Asn Arg Arg Arg Thr Ser Met
565 570 575

His Trp Ala Asn Arg Phe Asn Gln Pro Thr Gly Tyr Ala Ser Leu Pro
580 585 590

Thr Leu Ala Leu Leu Asn Glu Gln Gln Lys Glu Gln Glu His Lys Glu
595 600 605

Lys Gln Lys Gly Glu Asp Asp Gly Lys Val Ile Val Lys Thr Ile Ser
610 615 620

Ala Lys Thr Lys Ala Pro Ile Glu Val Ala Lys Ala Lys Ala Lys Thr
625 630 635 640

Cura 468 SEQ list 0705

Ser Ile Val Ile Thr Arg Pro Glu Ile Lys Asn Ala Lys Ala Lys Val
 645 650 655
 Asn Ser Phe Pro Val Gln Lys Ser Asn Thr Asn Gln Val Lys Lys Pro
 660 665 670
 Glu Lys Gln Glu Lys Ser Asp Thr Thr Ala Pro Ala Ala Ile Ala Ser
 675 680 685
 Ser Arg Leu Lys Met Thr Ser Leu His Lys Glu Tyr Met Arg Ser Glu
 690 695 700
 Lys Asn Ala Leu Arg Lys Leu Gln Gln Lys Glu Gln Gly Asn Gln Gln
 705 710 715 720
 His Asn Ser Ser Ser Ser Ser Ala Glu Thr Val Val Glu Ser Cys Asn
 725 730 735
 Glu Asp His Ser Lys Ile Asp Ile Lys Ile Gln Thr Asn Cys Glu Phe
 740 745 750
 Ser Lys Thr Ile Gly Glu Leu Tyr Glu Ser Ile Ala His Cys Lys Leu
 755 760 765
 Pro Ser Gly Ser Leu Lys Thr Asn Ala Ser Thr Leu Ser Ala Cys Asp
 770 775 780
 Glu Asn Glu Glu Gln Asn Thr Asp Asp Asn Glu Glu Glu Arg Asn Glu
 785 790 795 800
 Arg Ile Leu Gly Glu Val Gln Glu Ser Leu Glu Arg Gln Ile Arg Glu
 805 810 815
 Leu Glu Gln Thr Glu Ile Asp Val Asp Thr Glu Thr Asp Glu Thr Asp
 820 825 830
 Cys Glu Val Gln Leu Glu Glu Gln Asp Asp Gly Val Asp Gly Leu Glu
 835 840 845
 Met Gly Ser Gly Asp Asp Ser Ala Val Phe Val Thr Met Ser Asp Asp
 850 855 860
 Glu Asn Ala Ser Leu Glu Leu Arg Tyr Gln Ala Leu Leu Ser Asp Met
 865 870 875 880
 Ser Trp Asn Glu Arg Ala Glu Ala Leu Ala Thr Leu Gln Ala Tyr Val
 885 890 895
 Ala Arg His Pro Gly Arg Ala Gln Glu Leu His Gln Lys Leu Ser Ser
 900 905 910
 Pro Ser Arg Arg Arg Ser Leu Gln Glu Thr Leu Lys Lys Tyr Gln Ala
 915 920 925
 Lys Gln Ala Arg Ala Gln Gln Lys Arg Asn Leu Leu Gln Gln Glu Lys
 930 935 940
 Ala Ala Lys Leu Gln Gln Leu Phe Ser Arg Val Glu Asp Val Lys Ala
 945 950 955 960
 Ala Lys Asn Gln Ile Ile Glu Asp Lys Arg Gln Lys Met Gln Gly Arg
 965 970 975

Cura 468 SEQ list 0705

Leu Gln Arg Ala Ala Glu Asn Arg Glu Gln Tyr Leu Lys Gln Ile Ile
 980 985 990
 Glu Lys Ala His Asp Glu Glu Lys Lys Leu Lys Glu Ile Asn Phe Ile
 995 1000 1005
 Lys Asn Ile Glu Ala Gln Asn Lys Arg Leu Asp Leu Leu Glu Ser Ser
 1010 1015 1020
 Lys Glu Thr Glu Gly Arg Leu Gln Asp Leu Glu Gln Glu Arg Gln Lys
 1025 1030 1035 1040
 Arg Val Glu Glu Lys Leu Ala Lys Glu Ala Ala Val Glu Arg Arg Arg
 1045 1050 1055
 Gln Ala Leu Glu Lys Glu Arg Leu Leu Lys Leu Glu Lys Met Asn Glu
 1060 1065 1070
 Thr Arg Leu Glu Lys Glu Gln Arg Ile Gly Lys Met Gln Glu Gln Lys
 1075 1080 1085
 Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu
 1090 1095 1100
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu
 1105 1110 1115 1120
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His
 1125 1130 1135
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile
 1140 1145 1150
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu
 1155 1160 1165
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp
 1170 1175 1180
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg
 1185 1190 1195 1200
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys
 1205 1210 1215
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg
 1220 1225 1230
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly
 1235 1240 1245
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile
 1250 1255 1260
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly
 1265 1270 1275 1280
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn
 1285 1290 1295
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg
 1300 1305 1310

Cura 468 SEQ list 0705

Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly
1315 1320 1325

Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val
1330 1335 1340

Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp
1345 1350 1355 1360

Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg
1365 1370 1375

Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val
1380 1385 1390

Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser
1395 1400 1405

Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro
1410 1415 1420

Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu
1425 1430 1435 1440

Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn
1445 1450 1455

Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg
1460 1465 1470

Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly
1475 1480 1485

Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr
1490 1495 1500

Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr
1505 1510 1515 1520

Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln
1525 1530 1535

Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu
1540 1545 1550

Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn
1555 1560 1565

Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg
1570 1575 1580

Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu
1585 1590 1595 1600

Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr
1605 1610 1615

Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala
1620 1625 1630

Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp
1635 1640 1645

Cura 468 SEQ list 0705

Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu
 1650 1655 1660
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn
 1665 1670 1675 1680
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu
 1685 1690 1695
 Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp
 1700 1705 1710
 Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys
 1715 1720 1725
 Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val
 1730 1735 1740
 Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp
 1745 1750 1755 1760
 Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn
 1765 1770 1775
 Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala
 1780 1785 1790
 Gly Asn Lys Lys Asn Ala
 1795

<210> 49
 <211> 274
 <212> PRT
 <213> Toxocara canis

<400> 49

Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val
 1 5 10 15
 Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val
 20 25 30
 Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys
 35 40 45
 Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln
 50 55 60
 Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr
 65 70 75 80
 Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile
 85 90 95
 Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile
 100 105 110
 Gly Gln Asp Tyr Ala Glu Arg Val Leu Pro Ser Ile Thr Asn Glu Val
 115 120 125
 Leu Lys Ala Val Val Ala Gln Phe Asp Ala His Glu Met Ile Thr Gln
 130 135 140

Cura 468 SEQ list 0705

Arg Glu Ser Val Ser His Arg Val Ser Val Glu Leu Ser Glu Arg Ala
 145 150 155 160
 Arg Gln Phe Gly Ile Leu Leu Asp Asp Ile Ala Ile Thr His Leu Ser
 165 170 175
 Phe Gly Arg Glu Phe Thr Glu Ala Val Glu Met Lys Gln Val Ala Gln
 180 185 190
 Gln Glu Ala Glu Lys Ala Arg Tyr Leu Val Glu Thr Ala Glu Gln Met
 195 200 205
 Lys Ile Ala Ala Ile Thr Thr Ala Glu Gly Asp Ala Gln Ala Ala Lys
 210 215 220
 Leu Leu Ala Gln Ala Phe Lys Asp Ala Gly Asp Gly Leu Ile Glu Leu
 225 230 235 240
 Arg Lys Ile Glu Ala Ala Glu Glu Ile Ala Glu Arg Met Ser Lys Thr
 245 250 255
 Arg Asn Val Ile Tyr Leu Pro Gly Asn Gln Asn Thr Leu Phe Asn Leu
 260 265 270

Pro Ala

<210> 50
 <211> 402
 <212> PRT
 <213> Caenorhabditis elegans

<400> 50
 Met Glu Lys Tyr Lys Asn Glu Leu Glu Ile Phe Lys Arg Met Tyr Phe
 1 5 10 15
 Lys Asn Tyr Pro Thr Ser Ser Lys Asp Glu Glu Ala Ala Ala Val Ile
 20 25 30
 Gln Lys Gly Gly Glu Phe Ile Gln Glu Ile Leu Pro Thr Ile Ile Ser
 35 40 45
 Thr Ser Arg Ala Tyr Asp Thr Asn Gln Lys Ala Leu Leu Leu Ala Glu
 50 55 60
 Gly Gly Lys Met Tyr Asn Val Leu Glu Asp Tyr Asn Glu Thr Ala Glu
 65 70 75 80
 Lys Met Leu Ser Lys Ser Val Arg Met Asn Pro Lys Asn Ala Asp Ala
 85 90 95
 Trp His Glu Leu Gly Leu Cys Val Met Lys Arg Arg Asp Leu Glu Phe
 100 105 110
 Ala Gln Ser Cys Phe Lys Ile Ala Leu Gly Ile Ser Lys Thr Ala Pro
 115 120 125
 Ile Leu Thr Ser Leu Ala Val Ala Met Arg Leu Val Ala Leu Glu His
 130 135 140
 Pro Glu Pro Ala Gln Ala Glu Ile Arg Thr Lys Ala Met Glu Leu Ile

Cura 468 SEQ list 0705
155

145 150 160
 Ile Glu Ala Arg Arg Leu Asp Ser Ala Tyr Gly Pro Ala Asn Ile Ala
 165 170 175
 Phe Ala Thr Gly Leu Phe Tyr Cys Phe Phe Ser Thr Ala Lys Val Glu
 180 185 190
 Leu Lys Phe Leu Asp Lys Val Ile Glu Asn Tyr Lys Lys Ala Leu Glu
 195 200 205
 Cys Glu Leu Ser Arg Thr Asp Pro Gln Val Tyr Ile Asn Met Ala Thr
 210 215 220
 Cys Leu Lys Phe Met Glu Lys Tyr Asp Glu Ala Leu Ala Val Leu Gln
 225 230 235 240
 Lys Ala Val Glu Tyr Asp Pro Arg Asn Glu Leu Glu Thr Arg Glu Lys
 245 250 255
 Leu Ala Ser Phe Val Ser Tyr Leu Ser Lys Phe Thr Asp Ala Ile Gln
 260 265 270
 Lys Lys Gly Lys Met Lys Ala Lys Arg Met Gln Glu Met Ile Asn Glu
 275 280 285
 Leu Lys Lys Ser Ser Asp Gly Phe Arg Ala Lys Ile Ile Gly Asn Ile
 290 295 300
 Gly His Asp Glu Thr Ile Pro Val Ala Leu Val Gly Val Asp Ala Ala
 305 310 315 320
 Gly Glu Val Tyr Gly Ile Thr Ile Tyr Asn Cys Leu Ser Asn Phe Gly
 325 330 335
 Phe Val Ile Gly Asp Thr Val Thr Ile Ala Lys Pro Asp Phe Arg Glu
 340 345 350
 Ile Lys Asn Leu Thr Ile Pro Ser Asp Pro Glu Ile His Val Asp Ser
 355 360 365
 Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly
 370 375 380
 Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln
 385 390 395 400
 Thr Lys

<210> 51
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 51
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30

Cura 468 SEQ list 0705

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
210 215 220

Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
225 230 235 240

Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
245 250 255

Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
260 265 270

Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
275 280 285

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
290 295 300

Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
305 310 315 320

Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
325 330 335

Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
340 345 350

Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
355 360 365

Cura 468 SEQ list 0705

Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700

Cura 468 SEQ list 0705

His Lys Val Met Arg Leu Gly
705 710

<210> 52
<211> 711
<212> PRT
<213> Homo sapiens

<400> 52

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
1 5 10 15
Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30
Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45
Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60
Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80
Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95
Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110
Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125
Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140
Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160
Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175
Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190
Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205
Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
210 215 220
Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
225 230 235 240
Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
245 250 255
Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
260 265 270
Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
275 280 285

Cura 468 SEQ list 0705

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Phe Leu
 610 615 620

Cura 468 SEQ list 0705

Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
625 630 635 640
Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
645 650 655
Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
660 665 670
Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
675 680 685
Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
690 695 700
His Lys Val Met Arg Leu Gly
705 710

<210> 53
<211> 711
<212> PRT
<213> Homo sapiens

<400> 53
Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val
1 5 10 15
Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30
Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45
Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60
Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80
Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95
Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110
Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125
Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140
Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160
Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175
Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190
Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser

Cura 468 SEQ list 0705

195	200	205																	
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro				
	210					215					220								
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys				
225					230					235					240				
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro				
				245					250					255					
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala				
			260					265					270						
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly				
		275					280					285							
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys				
	290					295					300								
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu				
305					310					315					320				
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp				
				325					330					335					
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala				
			340					345					350						
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln				
		355					360					365							
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys				
	370					375					380								
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His				
385					390					395					400				
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu				
				405					410					415					
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr				
			420					425					430						
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys				
		435					440					445							
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln				
	450					455					460								
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser				
465					470					475					480				
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val				
				485					490					495					
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val				
			500					505					510						
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His				
		515					520					525							
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn				

Cura 468 SEQ list 0705
540

530

535

Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
545 550 555 560
Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
565 570 575
Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
580 585 590
Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
595 600 605
Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
610 615 620
Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
625 630 635 640
Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
645 650 655
Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
660 665 670
Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
675 680 685
Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
690 695 700
His Lys Val Met Arg Leu Gly
705 710

<210> 54
<211> 529
<212> PRT
<213> Homo sapiens

<400> 54

Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln
1 5 10 15
Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser
20 25 30
Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile
35 40 45
Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly
50 55 60
Gly Leu Ser Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Gln
65 70 75 80
Tyr Met Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn
85 90 95
Pro Asp Gly Asp Pro Gly Gly Pro Trp Cys His Thr Thr Asp Pro Ala
100 105 110

Cura 468 SEQ list 0705

Val Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Val Ala Ala Cys
 115 120 125
 Val Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu
 130 135 140
 Ser Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His
 145 150 155 160
 Pro Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr
 165 170 175
 Cys Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp
 180 185 190
 Pro Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu
 195 200 205
 Ala Gln Pro Arg Gln Glu Ala Thr Ser Val Ser Cys Phe Arg Gly Lys
 210 215 220
 Gly Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro
 225 230 235 240
 Cys Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro
 245 250 255
 Glu Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro
 260 265 270
 Asp Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg
 275 280 285
 Val Gly Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro
 290 295 300
 Gln Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser
 305 310 315 320
 Lys Thr Arg Lys Gly Val Gln Cys Gln Arg Gly Ser Ala Glu Thr Pro
 325 330 335
 His Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu
 340 345 350
 Glu Asn Phe Cys Gln Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala
 355 360 365
 Thr Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala
 370 375 380
 Ala Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys
 385 390 395 400
 Ser Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Val Val
 405 410 415
 Pro Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln
 420 425 430
 Ser Ala Cys Gly Ile Gly Gln Gly Gln His Phe Cys Gly Gly Ser Leu
 435 440 445

Cura 468 SEQ list 0705

Val Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys
 450 455 460
 His Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln
 465 470 475 480
 Asn Pro Gln His Gly Glu Pro Gly Leu Gln Arg Val Pro Val Ala Lys
 485 490 495
 Met Leu Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu
 500 505 510
 Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro
 515 520 525
 Glu

<210> 55
 <211> 716
 <212> PRT
 <213> Mus musculus

<400> 55
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Val Gln Cys Ser Arg Ala
 1 5 10 15
 Leu Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Leu Phe Arg Gly Thr
 20 25 30
 Glu Leu Arg Asn Leu Leu His Thr Ala Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Arg Arg Cys Gly Pro Leu Leu
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Met Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Leu His Thr Gln Leu Tyr His Ser Ser
 85 90 95
 Leu Cys His Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asp Asn Gly Val Ser Tyr Arg Gly Thr Val Ala Arg Thr Ala Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser Arg Arg Phe Pro Asn Asp His Lys Tyr
 130 135 140
 Thr Pro Thr Pro Lys Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160
 Asp Gly Asp Pro Arg Gly Pro Trp Cys Tyr Thr Thr Asn Arg Ser Val
 165 170 175
 Arg Phe Gln Ser Cys Gly Ile Lys Thr Cys Arg Glu Ala Val Cys Val
 180 185 190
 Leu Cys Asn Gly Glu Asp Tyr Arg Gly Glu Val Asp Val Thr Glu Ser
 195 200 205

Cura 468 SEQ list 0705

Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro
	210					215					220				
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu
			260					265					270		
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys
		275					280					285			
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr
	290					295					300				
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser
305					310					315					320
Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu
				325					330					335	
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys
			340					345					350		
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro
		355					360					365			
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly
	370					375					380				
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys
385					390					395					400
Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr
				405					410					415	
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp
			420					425					430		
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu
		435					440					445			
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser
	450					455					460				
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg
465					470					475					480
Val	Asp	Lys	Ser	Asn	Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn
				485					490					495	
Ser	Pro	Trp	Thr	Val	Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys
			500					505					510		
Gly	Gly	Ser	Leu	Val	Lys	Glu	Gln	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys
		515					520					525			
Ile	Trp	Ser	Cys	His	Glu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly
	530					535					540				

Cura 468 SEQ list 0705

Thr Ile Asn Gln Asn Pro Gln Pro Gly Glu Ala Asn Leu Gln Arg Val
545 550 555 560
Pro Val Ala Lys Ala Val Cys Gly Pro Ala Gly Ser Gln Leu Val Leu
565 570 575
Leu Lys Leu Glu Arg Pro Val Ile Leu Asn His His Val Ala Leu Ile
580 585 590
Cys Leu Pro Pro Glu Gln Tyr Val Val Pro Pro Gly Thr Lys Cys Glu
595 600 605
Ile Ala Gly Trp Gly Glu Ser Ile Gly Thr Ser Asn Asn Thr Val Leu
610 615 620
His Val Ala Ser Met Asn Val Ile Ser Asn Gln Glu Cys Asn Thr Lys
625 630 635 640
Tyr Arg Gly His Ile Gln Glu Ser Glu Ile Cys Thr Gln Gly Leu Val
645 650 655
Val Pro Val Gly Ala Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys
660 665 670
Tyr Thr His Asp Cys Trp Val Leu Gln Gly Leu Ile Ile Pro Asn Arg
675 680 685
Val Cys Ala Arg Pro Arg Trp Pro Ala Ile Phe Thr Arg Val Ser Val
690 695 700
Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu
705 710 715

<210> 56
<211> 135
<212> PRT
<213> Homo sapiens

<400> 56
Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30
Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp
35 40 45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr

115

120

125

Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 57
<211> 135
<212> PRT
<213> Homo sapiens

<400> 57

Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30

Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60

Phe Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110

Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125

Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 58
<211> 135
<212> PRT
<213> Homo sapiens

<400> 58

Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15

Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30

Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60

Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95

Cura 468 SEQ list 0705

His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys
100 105 110
Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr
115 120 125
Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 59
<211> 135
<212> PRT
<213> Homo sapiens

<400> 59
Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30
Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45
Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125
Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 60
<211> 135
<212> PRT
<213> Bos taurus

<400> 60
Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu
20 25 30
Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp
35 40 45
Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60

Cura 468 SEQ list 0705

Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu
100 105 110
Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125
Arg Val Tyr Glu Lys Val Glu
130 135

<210> 61
<211> 266
<212> PRT
<213> Homo sapiens

<400> 61

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15
Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
20 25 30
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
35 40 45
Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
130 135 140
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
210 215 220

Cura 468 SEQ list 0705

Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
 225 230 235 240
 Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
 245 250 255
 Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
 260 265

<210> 62
 <211> 265
 <212> PRT
 <213> Rattus norvegicus

<400> 62
 Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45
 Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60
 Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asp
 100 105 110
 Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
 130 135 140
 Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160
 Val Val Ala Cys Ser Val Gln Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175
 Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Ala Tyr Leu
 195 200 205
 Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Gln Lys Thr
 210 215 220
 Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
 225 230 235 240
 Lys Gly His Pro Gln Asp Glu Ser Thr Val Leu Thr Lys Ala Gly Met

245

255

Ala Thr Val Asp Ala Gly Val Tyr Pro
260 265

<210> 63
<211> 266
<212> PRT
<213> Mus musculus

<400> 63

Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
1 5 10 15

Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Asp Gln
35 40 45

Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn
100 105 110

Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
130 135 140

Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160

Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175

Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu
195 200 205

Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala
210 215 220

Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
225 230 235 240

Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly
245 250 255

Met Ala Thr Val Asp Ala Gly Val Tyr Pro
260 265

Cura 468 SEQ list 0705

<210> 64
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 35 40 45
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
 50 55 60
 Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
 100 105 110
 Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
 130 135 140
 Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
 145 150 155 160
 Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
 165 170 175
 Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
 195 200 205
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
 210 215 220
 Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
 225 230 235 240
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
 245 250 255
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
 260 265 270
 Leu

<210> 65

Cura 468 SEQ list 0705

<211> 273
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (41)
 <223> wherein Xaa is any amino acid.

<400> 65

```

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1          5          10          15
Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
          20          25          30
Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His
          35          40          45
Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
          50          55          60
Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65          70          75          80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
          85          90          95
Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
          100          105          110
Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
          115          120          125
Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
          130          135          140
Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145          150          155          160
Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
          165          170          175
Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
          180          185          190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
          195          200          205
Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
          210          215          220
Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225          230          235          240
Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
          245          250          255
Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
          260          265          270
Leu
    
```


Cura 468 SEQ list 0705

<210> 66
 <211> 434
 <212> PRT
 <213> Homo sapiens

<400> 66

Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys
 1 5 10 15
 Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys
 20 25 30
 His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met
 35 40 45
 Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala
 50 55 60
 Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly
 65 70 75 80
 Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met
 85 90 95
 Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro
 100 105 110
 Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr
 115 120 125
 Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr
 130 135 140
 Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys
 145 150 155 160
 Pro Gln Ser Pro Pro Leu Thr Pro Thr Ser Leu Phe Thr Ser Ser Thr
 165 170 175
 Pro Asn Gly Ser Gln Phe Leu Thr Phe Ser Ile Glu Pro Val His Tyr
 180 185 190
 Cys Met Asn Glu Ile Lys Thr Gly Lys Pro Arg Ile Pro Ser Phe Arg
 195 200 205
 Ser Leu Lys Arg Gly Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro
 210 215 220
 Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn
 225 230 235 240
 Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met
 245 250 255
 Lys Asp Val Tyr Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu
 260 265 270
 Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met
 275 280 285
 Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr

Cura 468 SEQ list 0705
300

290

295

Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val
305 310 315 320
Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn
325 330 335
Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe
340 345 350
Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys
355 360 365
Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met
370 375 380
Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly
385 390 395 400
Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr
405 410 415
Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ala Val Thr
420 425 430
Tyr Ile

<210> 67
<211> 330
<212> PRT
<213> Homo sapiens

<400> 67

Met Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe
1 5 10 15
Ala Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu
20 25 30
Gly Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln
35 40 45
Met Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe
50 55 60
Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly
65 70 75 80
Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr
85 90 95
Thr Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro
100 105 110
Lys Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg
115 120 125
Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln
130 135 140

Cura 468 SEQ list 0705

Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr
 145 150 155 160
 Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu
 165 170 175
 Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys
 180 185 190
 Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly
 195 200 205
 Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg
 210 215 220
 Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn Gln Glu Val Arg
 225 230 235 240
 Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe Asp Asp Glu Phe
 245 250 255
 Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys Lys Ala Ile Tyr
 260 265 270
 Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met Lys Glu Gly Glu
 275 280 285
 Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala
 290 295 300
 Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp
 305 310 315 320
 Val Thr Leu Glu Lys Asn Ser Lys Gly Ser
 325 330

<210> 68
 <211> 592
 <212> PRT
 <213> Homo sapiens

<400> 68

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys
 1 5 10 15
 His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val
 20 25 30
 Lys Glu Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn
 35 40 45
 Leu Ser Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu
 50 55 60
 Tyr Lys Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met
 65 70 75 80
 Asn Asp Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser
 85 90 95
 Gln Ile Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu
 100 105 110

Cura 468 SEQ list 0705

Arg Lys Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu
 115 120 125
 Thr Cys Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp
 130 135 140
 Cys Lys Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala
 145 150 155 160
 Asp Ile Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala
 165 170 175
 Gln Ile Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser
 180 185 190
 Ile Leu Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His
 195 200 205
 Ile Pro Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile
 210 215 220
 Val Arg Met Gly Glu Ser Met Lys Thr Tyr Ala Glu Val Asp Arg Gln
 225 230 235 240
 Val Ile Pro Ile Ile Gly Lys Cys Leu Asp Gly Ile Val Lys Ala Ala
 245 250 255
 Glu Ser Ile Asp Gln Lys Asn Asp Ser Gln Leu Val Ile Glu Ala Tyr
 260 265 270
 Lys Ser Gly Phe Glu Pro Pro Gly Asp Ile Glu Phe Glu Asp Tyr Thr
 275 280 285
 Gln Pro Met Lys Arg Thr Val Ser Asp Asn Ser Leu Ser Asn Ser Arg
 290 295 300
 Gly Glu Gly Lys Pro Asp Leu Lys Phe Gly Gly Lys Ser Lys Gly Lys
 305 310 315 320
 Leu Trp Pro Phe Ile Lys Lys Asn Lys Ser Pro Lys Gln Gln Lys Glu
 325 330 335
 Pro Leu Ser His Arg Phe Asn Glu Phe Met Thr Ser Lys Pro Lys Ile
 340 345 350
 His Cys Phe Arg Ser Leu Lys Arg Gly Leu Ser Leu Lys Leu Gly Ala
 355 360 365
 Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro Glu Gln Arg Arg Lys Lys
 370 375 380
 Leu Gln Gln Lys Val Asp Glu Leu Asn Lys Glu Ile Gln Lys Glu Met
 385 390 395 400
 Asp Gln Arg Asp Ala Ile Thr Lys Met Lys Asp Val Tyr Leu Lys Asn
 405 410 415
 Pro Gln Met Gly Asp Pro Ala Ser Leu Asp His Lys Leu Ala Glu Val
 420 425 430
 Ser Gln Asn Ile Glu Lys Leu Arg Val Glu Thr Gln Lys Phe Glu Ala
 435 440 445

Cura 468 SEQ list 0705

Trp Leu Ala Glu Val Glu Gly Arg Leu Pro Ala Arg Asn Glu Gln Ala
450 455 460
Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln Asn Pro Pro Thr Val Asn
465 470 475 480
Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp Gly Ser Tyr Thr Glu Glu
485 490 495
Gln Ser Gln Glu Ser Glu Met Lys Val Leu Ala Thr Asp Phe Asp Asp
500 505 510
Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala
515 520 525
Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu
530 535 540
Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr
545 550 555 560
Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr
565 570 575
Val Glu Val Cys Leu Asp Lys Asn Ala Lys Gly Ala Lys Thr Tyr Ile
580 585 590

<210> 69
<211> 679
<212> PRT
<213> Homo sapiens

<400> 69
Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg
1 5 10 15
Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser
20 25 30
Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu
35 40 45
Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser
50 55 60
Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr
65 70 75 80
Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu
85 90 95
Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser
100 105 110
Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys
115 120 125
Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp

Cura 468 SEQ list 0705
140

130		135															
Tyr	Ala	Gly	Gln	His	Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile		
145					150					155					160		
Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys		
				165					170					175			
Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys		
			180					185					190				
Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys		
		195					200					205					
Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile		
	210					215					220						
Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile		
225					230					235					240		
Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu		
				245					250					255			
Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro		
			260					265					270				
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg		
		275					280					285					
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile		
	290					295					300						
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser		
305					310					315					320		
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser		
				325					330					335			
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro		
			340					345					350				
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu		
		355					360					365					
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp		
	370					375					380						
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His		
385					390					395					400		
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro		
				405					410					415			
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg		
			420				425						430				
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser		
	435						440					445					
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe		
	450					455					460						
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val		

Cura 468 SEQ list 0705
475

465 470 480
Asp Glu Leu Asn Lys Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala
 485 490 495
Ile Thr Lys Met Lys Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp
 500 505 510
Pro Ala Ser Leu Asp His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu
 515 520 525
Lys Leu Arg Val Glu Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val
 530 535 540
Glu Gly Arg Leu Pro Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly
545 550 555
Leu Tyr Asp Ser Gln Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp
 565 570 575
Arg Glu Ser Pro Asp Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser
 580 585 590
Glu Met Lys Val Leu Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu
 595 600 605
Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu
 610 615 620
Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr
625 630 635
Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn
 645 650 655
Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu
 660 665 670
Asp Lys Asn Ala Lys Asp Ser
 675

<210> 70
<211> 674
<212> PRT
<213> Homo sapiens

<400> 70
Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu
1 5 10 15
Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly
 20 25 30
Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg
 35 40 45
Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu
 50 55 60
Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr Gln Trp Gly Ile Asp
65 70 75 80

Cura 468 SEQ list 0705

Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu Arg Thr Glu Ile Glu
 85 90 95
 Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser Lys Lys Tyr Gln Pro
 100 105 110
 Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys Tyr Thr Ser Cys Lys
 115 120 125
 Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp Tyr Ala Gly Gln His
 130 135 140
 Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile Ile Val Asp Leu Ala
 145 150 155 160
 Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys Ser Asn Phe His Asp
 165 170 175
 Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys Trp Lys Gln Leu Glu
 180 185 190
 Ser Ser Lys Arg Arg Phe Glu Arg Asp Cys Lys Glu Ala Asp Arg Ala
 195 200 205
 Gln Gln Tyr Phe Glu Lys Met Asp Ala Asp Ile Asn Val Thr Lys Ala
 210 215 220
 Asp Val Glu Lys Ala Arg Gln Gln Ala Gln Ile Arg His Gln Met Ala
 225 230 235 240
 Glu Asp Ser Lys Ala Asp Tyr Ser Ser Ile Leu Gln Lys Phe Asn His
 245 250 255
 Glu Gln His Glu Tyr Tyr His Thr His Ile Pro Asn Ile Phe Gln Lys
 260 265 270
 Ile Gln Glu Met Glu Glu Arg Arg Ile Val Arg Met Gly Glu Ser Met
 275 280 285
 Lys Thr Tyr Ala Glu Val Asp Arg Gln Val Ile Pro Ile Ile Gly Lys
 290 295 300
 Cys Leu Asp Gly Ile Val Lys Ala Ala Glu Ser Ile Asp Gln Lys Asn
 305 310 315 320
 Asp Ser Gln Leu Val Ile Glu Ala Tyr Lys Ser Gly Phe Glu Pro Pro
 325 330 335
 Gly Asp Ile Glu Phe Glu Asp Tyr Thr Gln Pro Met Lys Arg Thr Val
 340 345 350
 Ser Asp Asn Ser Leu Ser Asn Ser Arg Gly Glu Gly Lys Pro Asp Leu
 355 360 365
 Lys Phe Gly Gly Lys Ser Lys Gly Lys Leu Trp Pro Phe Ile Lys Lys
 370 375 380
 Asn Lys Leu Met Ser Leu Leu Thr Ser Pro His Gln Pro Pro Pro Pro
 385 390 395 400
 Pro Pro Ala Ser Ala Ser Pro Ser Ala Val Pro Asn Gly Pro Gln Ser
 405 410 415

Cura 468 SEQ list 0705

Pro Lys Gln Gln Lys Glu Pro Leu Ser His Arg Phe Asn Glu Phe Met
420 425 430

Thr Ser Lys Pro Lys Ile His Cys Phe Arg Ser Leu Lys Arg Gly Leu
435 440 445

Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro
450 455 460

Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu Leu Asn Lys
465 470 475 480

Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr Lys Met Lys
485 490 495

Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala Ser Leu Asp
500 505 510

His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu Arg Val Glu
515 520 525

Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly Arg Leu Pro
530 535 540

Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln
545 550 555 560

Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp
565 570 575

Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met Lys Val Leu
580 585 590

Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala
595 600 605

Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly
610 615 620

Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp
625 630 635 640

Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly
645 650 655

Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys Asn Ala Lys
660 665 670

Asp Ser

<210> 71
<211> 457
<212> PRT
<213> Homo sapiens

<400> 71
Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
1 5 10 15
Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
20 25 30

Cura 468 SEQ list 0705

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220
 Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240
 His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255
 Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270
 Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285
 Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu
 355 360 365

Cura 468 SEQ list 0705

Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu
 370 375 380
 Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr
 405 410 415
 Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro
 420 425 430
 Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Ala Gln Asp Ser Leu Leu
 450 455

<210> 72
 <211> 455
 <212> PRT
 <213> Mus musculus

<400> 72
 Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr
 1 5 10 15
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln
 20 25 30
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly
 35 40 45
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro Ala Ala Ser Pro Ser Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Glu Glu Glu Met Thr Leu Asn Cys Pro Gly Val
 85 90 95
 Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln Val Gln Val Arg Ala Arg
 115 120 125
 Pro Asp Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
 145 150 155 160
 Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
 180 185 190
 Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu

205

Cura 468 SEQ list 0705

Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu
 35 40 45
 Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro
 50 55 60
 Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr
 65 70 75 80
 Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu
 85 90 95
 Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln
 100 105 110
 Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly
 115 120 125
 Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile
 130 135 140
 Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn
 145 150 155 160
 Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala Arg Pro Gly Gly Leu Val
 165 170 175
 Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys Pro Ser Gly Arg Ile Val
 180 185 190
 Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile
 195 200 205
 Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser
 210 215 220
 Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala Pro
 225 230 235 240
 His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu Ser
 245 250 255
 Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly Ala
 260 265 270
 Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His Pro
 275 280 285
 Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln Leu
 290 295 300
 Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro
 305 310 315 320
 Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser Gly
 325 330 335
 Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu Gln
 340 345 350
 Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser Cys
 355 360 365

Cura 468 SEQ list 0705

Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr Leu
 370 375 380
 Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 385 390 395 400
 Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp Gly
 405 410 415
 Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val Ala
 420 425 430
 Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
 435 440 445

<210> 74
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 74
 Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15
 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30
 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Cura 468 SEQ list 0705

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240
 His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255
 Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270
 Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285
 Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu
 355 360 365
 Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro
 370 375 380
 His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly
 385 390 395

<210> 75
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 75
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
 1 5 10 15
 Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
 20 25 30
 Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
 35 40 45
 Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu
 50 55 60
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
 65 70 75 80
 Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
 85 90 95
 His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
 100 105 110
 Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg

Cura 468 SEQ list 0705

115	120	125
Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly		
130	135	140
Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn		
145	150	155
His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe		
	165	170
Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe		
	180	185
Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro		
	195	200
Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu		
	210	215
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu		
	225	230
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala		
	245	250
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr		
	260	265
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro		
	275	280
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile		
	295	300
His Asp Thr Val Gln Val Arg		
305	310	

<210> 76
 <211> 199
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reprolysin
 family zinc protease Consensus Sequence

<400> 76
 Lys Tyr Ile Glu Leu Phe Ile Val Val Asp His Gly Met Phe Thr Lys
 1 5 10 15
 Tyr Gly Ser Asp Leu Asn Lys Ile Arg Gln Arg Val His Gln Ile Val
 20 25 30
 Asn Leu Val Asn Glu Ile Tyr Arg Pro Leu Asn Ile Arg Val Val Leu
 35 40 45
 Val Gly Leu Glu Ile Trp Ser Asp Gly Asp Lys Ile Thr Val Gln Gly
 50 55 60
 Asp Ala Asn Asp Thr Leu His Arg Phe Leu Glu Trp Arg Glu Thr Asp
 65 70 75 80

Cura 468 SEQ list 0705

Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Gly Ile
85 90 95
Asp Phe Asp Gly Asn Thr Ile Gly Ala Ala Tyr Val Gly Gly Met Cys
100 105 110
Ser Pro Lys Arg Ser Val Gly Val Val Gln Asp His Ser Pro Ile Val
115 120 125
Leu Leu Val Ala Val Thr Met Ala His Glu Leu Gly His Asn Leu Gly
130 135 140
Met Thr His Asp Asp Ile Asn Lys Cys Thr Cys Glu Gly Gly Gly Gly
145 150 155 160
Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser
165 170 175
Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro
180 185 190
Gln Cys Leu Leu Asn Lys Pro
195

<210> 77
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 Consensus Sequence

<400> 77
Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly
1 5 10 15
Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly
20 25 30
Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln
35 40 45
Pro Cys Pro
50

<210> 78
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 domain Consensus Sequence

<400> 78
Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly
1 5 10 15
Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro

20

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys
35 40 45

<210> 79
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reprolysin
family propeptide Consensus Sequence

<400> 79
His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr
1 5 10 15
Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln
20 25 30
Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala
35 40 45
Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu
50 55 60
Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu
65 70 75 80
His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys
85 90 95
Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile
100 105 110
Arg Ser Pro Ser Pro
115

<210> 80
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Alpha-2-macroglobulin family Consensus Sequence

<400> 80
Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu Ser Trp
1 5 10 15
Leu Trp Glu Val Glu Glu Val Asp Arg Ser Pro Val Leu Thr Val Asn
20 25 30
Ile Thr Leu Pro Asp Ser Ile Thr Thr Trp Glu Ile Leu Ala Val Ser
35 40 45

Cura 468 SEQ list 0705

Leu Ser Asn Thr Lys Gly Leu Cys Val Ala Asp Pro Val Glu Leu Thr
 50 55 60
 Val Phe Gln Asp Phe Phe Leu Glu Leu Arg Leu Pro Tyr Ser Val Val
 65 70 75 80
 Arg Gly Glu Gln Val Glu Leu Arg Ala Val Leu Tyr Asn Tyr Leu Pro
 85 90 95
 Ser Gln Asp Ile Lys Val Val Val Gln Leu Glu Val Glu Pro Leu Cys
 100 105 110
 Gln Ala Gly Phe Cys Ser Leu Ala Thr Gln Arg Thr Arg Ser Ser Gln
 115 120 125
 Ser Val Arg Pro Lys Ser Leu Ser Ser Val Ser Phe Pro Val Val Val
 130 135 140
 Val Pro Leu Ala Ser Gly Leu Ser Leu Val Glu Val Val Ala Ser Val
 145 150 155 160
 Pro Glu Phe Phe Val Lys Asp Ala Val Val Lys Thr Leu Lys Val Glu
 165 170 175
 Pro Glu Gly Ala Arg Lys Glu Glu Thr Val Ser Ser Leu Leu Leu Pro
 180 185 190
 Pro Glu His Leu Gly Gly Gly Leu Glu Val Ser Glu Val Pro Ala Leu
 195 200 205
 Lys Leu Pro Asp Asp Val Pro Asp Thr Glu Ala Glu Ala Val Ile Ser
 210 215 220
 Val Gln Gly Asp Pro Val Ala Gln Ala Ile Gln Asn Thr Leu Ser Gly
 225 230 235 240
 Glu Gly Leu Asn Asn Leu Leu Arg Leu Pro Ser Gly Cys Gly Glu Gln
 245 250 255
 Asn Met Ile Tyr Met Ala Pro Thr Val Tyr Val Leu His Tyr Leu Asp
 260 265 270
 Glu Thr Trp Gln Trp Glu Lys Pro Gly Thr Lys Lys Lys Gln Lys Ala
 275 280 285
 Ile Asp Leu Ile Asn Lys Gly Tyr Gln Arg Gln Leu Asn Tyr Arg Lys
 290 295 300
 Ala Asp Gly Ser Tyr Ala Ala Phe Leu His Arg Ala Ser Ser Thr Trp
 305 310 315 320
 Leu Thr Ala Phe Val Leu Lys Val Phe Ser Gln Ala Arg Asn Tyr Val
 325 330 335
 Phe Ile Asp Glu Glu His Ile Cys Gly Ala Val Lys Trp Leu Ile Leu
 340 345 350
 Asn Gln Gln Lys Asp Asp Gly Val Phe Arg Glu Ser Gly Pro Val Ile
 355 360 365
 His Asn Glu Met Lys Gly Gly Val Gly Asp Asp Ala Glu Val Glu Val
 370 375 380

Cura 468 SEQ list 0705

Thr 385 Leu Thr Ala Phe 390 Ile Thr Ile Ala 395 Leu Leu Glu Ala Lys Leu Val 400
 Cys Ile Ser Pro Val 405 Val Ala Asn Ala 410 Leu Ser Ile Leu Lys Ala 415 Ser
 Asp Tyr Leu 420 Leu Glu Asn Tyr Ala 425 Asn Gly Gln Arg Val 430 Tyr Thr Leu
 Ala Leu 435 Thr Ala Tyr Ala 440 Leu Ala Leu Ala Gly Val 445 Leu His Lys Leu
 Lys Glu 450 Ile Leu Lys Ser 455 Leu Lys Glu Glu Leu Tyr 460 Lys Ala Leu Val
 Lys 465 Gly His Trp Glu Arg 470 Pro Gln Lys Pro 475 Lys Asp Ala Pro Gly His 480
 Pro Tyr Ser Pro 485 Gln Pro Gln Ala Ala 490 Ala Val Glu Met Thr 495 Ser Tyr
 Ala Leu Leu 500 Ala Leu Leu Thr Leu 505 Leu Pro Phe Pro Lys 510 Val Glu Met
 Ala Pro 515 Lys Val Val Lys Trp 520 Leu Thr Glu Gln Gln 525 Tyr Tyr Gly Gly
 Gly Phe 530 Gly Ser Thr Gln 535 Asp Thr Val Met Ala 540 Leu Gln Ala Leu Ser
 Lys 545 Tyr Gly Ile Ala 550 Thr Pro Thr His Lys 555 Glu Lys Asn Leu Ser Val 560
 Thr Ile Gln Ser 565 Pro Ser Gly Ser Phe 570 Lys Ser His Phe Gln 575 Ile Leu
 Asn Asn Asn 580 Ala Phe Leu Leu Arg 585 Pro Val Glu Leu Pro 590 Leu Asn Glu
 Gly Phe 595 Thr Val Thr Ala Lys 600 Val Thr Gly Gln Gly 605 Thr Leu Thr Leu
 Val 610 Thr Thr Tyr Arg Tyr 615 Lys Val Leu Asp Lys 620 Lys Asn Thr Phe Cys
 Phe 625 Asp Leu Lys Ile 630 Glu Thr Val Pro Asp Thr 635 Cys Val Glu Pro Lys 640
 Gly Ala Lys Asn 645 Ser Asp Tyr Leu Ser 650 Ile Cys Thr Arg Tyr Ala 655 Gly
 Ser Arg Ser 660 Asp Ser Gly Met Ala 665 Ile Ala Asp Ile Ser 670 Met Leu Thr
 Gly Phe 675 Ile Pro Leu Lys Pro 680 Asp Leu Lys Lys Leu 685 Glu Asn Gly Val
 Asp 690 Arg Tyr Val Ser Lys 695 Tyr Glu Ile Asp Gly 700 Asn His Val Leu Leu
 Tyr 705 Leu Asp Lys Val 710 Ser His Ser Glu Thr 715 Glu Cys Val Gly Phe 720 Lys

Cura 468 SEQ list 0705

Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys
725 730 735

Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr
740 745 750

<210> 81

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family N-terminal region
Consensus Sequence

<400> 81

Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser
1 5 10 15

Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr
20 25 30

Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr
35 40 45

Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu
50 55 60

Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys
65 70 75 80

Val Ser Phe Thr Val Pro Gln Pro Gly Leu Phe Lys Ser Ser Lys Gly
85 90 95

Glu Glu Ser Phe Val Val Val Gln Val Lys Gly Pro Thr His Thr Phe
100 105 110

Lys Glu Lys Val Thr Val Leu Val Ser Ser Arg Arg Gly Leu Val Phe
115 120 125

Ile Gln Thr Asp Lys Pro Ile Tyr Thr Pro Gly Gln Thr Val Arg Tyr
130 135 140

Arg Val Phe Ser Val Asp Glu Asn Leu Arg Pro Leu Asn Glu Leu Ile
145 150 155 160

Leu Val Tyr Ile Glu Asp Pro Glu Gly Asn Arg Val Asp Gln Trp Glu
165 170 175

Val Asn Lys Leu Glu Gly Gly Ile Phe Gln Leu Ser Phe Pro Ile Pro
180 185 190

Ser Glu Pro Ile Gln Gly Thr Trp Lys Ile Val Ala Arg Tyr Glu Ser
195 200 205

Gly Pro Glu Ser Asn Tyr Thr His Tyr Phe Glu Val Lys Glu Tyr Val
210 215 220

Leu Pro Ser Phe Glu Val Ser Ile Thr Pro Pro Lys Pro Phe Ile Tyr
225 230 235 240

Cura 468 SEQ list 0705

Tyr Asp Asn Phe Lys Glu Phe Glu Val Thr Ile Cys Ala Arg Tyr Thr
 245 250 255
 Tyr Gly Lys Pro Val Pro Gly Val Ala Tyr Val Arg Phe Gly Val Lys
 260 265 270
 Asp Glu Asp Gly Lys Lys Glu Leu Leu Ala Gly Leu Glu Glu Arg Ala
 275 280 285
 Lys Leu Leu Asp Gly Asn Gly Glu Ile Cys Leu Ser Gln Glu Val Leu
 290 295 300
 Leu Lys Glu Leu Gln Leu Lys Asn Glu Asp Leu Glu Gly Lys Ser Leu
 305 310 315 320
 Tyr Val Ala Val Ala Val Ile Glu Ser Glu Gly Gly Asp Met Glu Glu
 325 330 335
 Ala Glu Leu Gly Gly Ile Lys Ile Val Arg Ser Pro Tyr Lys Leu Lys
 340 345 350
 Phe Val Lys Thr Pro Ser His Phe Lys Pro Gly Ile Pro Phe Phe Leu
 355 360 365
 Lys Val Leu Val Val Asp Pro Asp Gly Ser Pro Ala Pro Asn Val Pro
 370 375 380
 Val Lys Val Ser Ala Gln Asp Ala Ser Tyr Tyr Ser Asn Gly Thr Thr
 385 390 395 400
 Asp Glu Asp Gly Leu Ala Gln Phe Ser Ile Asn Thr Ser Gly Ile Ser
 405 410 415
 Ser Leu Ser Ile Thr Val Arg Thr Asn His Lys Glu Leu Pro Glu Glu
 420 425 430
 Val Gln Ala His Ala Glu Ala Gln Ala Thr Ala Tyr Ser Thr Val Ser
 435 440 445
 Leu Ser Lys Ser Tyr Ile His Leu Ser Ile Glu Arg Thr Leu Pro Cys
 450 455 460
 Gly Pro Gly Val Gly Glu Gln Ala Asn Phe Ile Leu Arg Gly Lys Ser
 465 470 475 480
 Leu Gly Glu Leu Lys Ile Leu His Phe Tyr Tyr Leu Ile Met Ser Lys
 485 490 495
 Gly Lys Ile Val Lys Thr Gly Arg Glu Pro Arg Glu Pro Gly Gln Gly
 500 505 510
 Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe
 515 520 525
 Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp
 530 535 540
 Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu
 545 550 555 560
 Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys
 565 570 575

Cura 468 SEQ list 0705

Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val
580 585 590
Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser
595 600 605
Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly
610 615 620

<210> 82
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sodium Bile
acid symporter family consensus sequence

<400> 82
Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg
1 5 10 15
Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu
20 25 30
Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu
35 40 45
Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile
50 55 60
Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr
65 70 75 80
Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser
85 90 95
Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala
100 105 110
Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys
115 120 125
Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr
130 135 140
Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu
145 150 155 160
Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe
165 170 175
Ala Leu Asn Gly Glu Val Ile Ala Ser Leu
180 185

<210> 83
<211> 191
<212> PRT
<213> Artificial Sequence

<220>

Cura 468 SEQ list 0705

<223> Description of Artificial Sequence: SPFH
domain/Band 7 family Consensus Sequence

<400> 83

```

Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val
 1          5          10          15
Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg
 20          25          30
Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe
 35          40          45
Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val
 50          55          60
Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp
 65          70          75          80
Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu
 85          90          95
Val Glu Asp Ala Glu Arg Ala Leu Pro Gln Leu Ala Gln Thr Thr Leu
100          105          110
Arg Asn Val Ile Gly Gln Phe Thr Leu Asp Glu Ile Leu Thr Glu Arg
115          120          125
Glu Arg Ile Asn Ser Gln Leu Arg Glu Ile Leu Asp Glu Ala Thr Asp
130          135          140
Pro Trp Gly Ile Lys Val Glu Arg Val Glu Ile Lys Asp Ile Arg Leu
145          150          155          160
Pro Glu Glu Val Gln Arg Ala Met Ala Ala Gln Met Glu Ala Glu Arg
165          170          175
Glu Ala Arg Ala Lys Ile Leu Glu Ala Glu Gly Glu Gln Glu Ala
180          185          190

```

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin
homologues Consensus Sequence

<400> 84

```

Ala Ala Phe Tyr Val Ile Gly Glu Gly Glu Arg Gly Val Val Glu Arg
 1          5          10          15
Leu Gly Arg Val Leu Lys Val Leu Gly Pro Gly Leu His Phe Val Ile
 20          25          30
Pro Phe Ile Asp Asp Val Lys Arg Val Asp Leu Arg Ala Gln Thr Asp
 35          40          45
Asp Val Pro Pro Gln Glu Val Ile Thr Lys Asp Asn Val Thr Val Ser
 50          55          60

```


Cura 468 SEQ list 0705

Val Asp Ala Val Val Tyr Tyr Arg Val Leu Asp Pro Leu Lys Ala Val
65 70 75 80
Tyr Gly Val Leu Asp Ala Asp Tyr Arg Ala Leu Arg Gln Leu Ala Gln
85 90 95
Thr Thr Leu Arg Ser Val Ile Gly Lys Arg Thr Leu Asp Glu Leu Leu
100 105 110
Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn
115 120 125
Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys
130 135 140
Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln
145 150 155 160

<210> 85
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 85
Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr
1 5 10 15
Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg
20 25 30
His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu
35 40 45
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr
50 55 60
Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys
65 70 75

<210> 86
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 86
Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser
1 5 10 15
Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro
20 25 30

Cura 468 SEQ list 0705

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu
35 40 45
His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys
50 55 60
Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln
65 70 75 80
Cys Glu Ser

<210> 87
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 87
Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15
Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
20 25 30
Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
35 40 45
Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
50 55 60
Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
65 70 75 80
Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
85 90 95
Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
100 105 110
Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
115 120 125
Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
130 135 140
Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
145 150 155 160
Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
165 170 175
Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
180 185 190
Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
195 200 205

Cura 468 SEQ list 0705

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
210 215 220

Ser Tyr Leu Asp Trp Ile
225 230

<210> 88
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trypsin
Consensus Sequence

<400> 88
Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
1 5 10 15
Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
20 25 30
Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
35 40 45
Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
50 55 60
Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
65 70 75 80
Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
85 90 95
Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
100 105 110
Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
115 120 125
Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
130 135 140
Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
145 150 155 160
Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
165 170 175
Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
180 185 190
Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
195 200 205
Arg Val Ser Arg Tyr Leu Asp Trp Ile
210 215

<210> 89
<211> 79
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Divergent
subfamily of APPLE domains Consensus Sequence

<400> 89

```

Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp
 1          5          10          15
Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln
          20          25          30
Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn
          35          40          45
Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala
 50          55          60
Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile
 65          70          75

```

<210> 90

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Lipocalin/cytosolic fatty-acid binding protein
family Consensus Sequence

<400> 90

```

Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro
 1          5          10          15
Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile
          20          25          30
Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys
          35          40          45
Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys
 50          55          60
Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val
 65          70          75          80
Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly
          85          90          95
Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro
          100          105          110
Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu
          115          120          125
Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg
 130          135          140

```

Cys
145

Cura 468 SEQ list 0705

<210> 91
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Connexin
 Consensus Sequence

<400> 91
 Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His
 1 5 10 15
 Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg
 20 25 30
 Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln
 35 40 45
 Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys
 50 55 60
 Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln
 65 70 75 80
 Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala
 85 90 95
 Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His
 100 105 110
 Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu
 115 120 125
 Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe
 130 135 140
 Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln
 145 150 155 160
 Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg
 165 170 175
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu
 180 185 190
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu
 195 200 205
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu
 210 215

<210> 92
 <211> 59
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Src homology 3
 domains Consensus Sequence

Cura 468 SEQ list 0705

<400> 92

Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro
 1 5 10 15
 Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys
 20 25 30
 Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly
 35 40 45
 Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp
 50 55

<210> 93

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SH3 domain
 Consensus Sequence

<400> 93

Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu
 1 5 10 15
 Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp
 20 25 30
 Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu
 35 40 45
 Ile Pro Ser Asn Tyr Val Glu Pro Val
 50 55

<210> 94

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
 homology domain Consensus Sequence

<400> 94

Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser
 1 5 10 15
 Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met
 20 25 30
 Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys
 35 40 45
 Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly
 50 55 60
 Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu
 65 70 75 80

Cura 468 SEQ list 0705

Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu
85 90

<210> 95
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fes/CIP4
homology domain Consensus Sequence

<400> 95
Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu
1 5 10 15
Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe
20 25 30
Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln
35 40 45
His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu
50 55 60
Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr
65 70 75 80
Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu
85 90

<210> 96
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 96
Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15
Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
20 25 30
Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
35 40 45
Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
50 55 60
Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
65 70 75 80
Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
85 90 95
Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
100 105 110

Cura 468 SEQ list 0705

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
115 120 125
Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
130 135 140
Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
145 150 155 160
Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
165 170 175
Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
180 185 190
Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
195 200 205
Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
210 215 220
Ser Tyr Leu Asp Trp Ile
225 230

<210> 97
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trypsin
Consensus Sequence

<400> 97
Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
1 5 10 15
Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
20 25 30
Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
35 40 45
Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
50 55 60
Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
65 70 75 80
Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
85 90 95
Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
100 105 110
Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
115 120 125
Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
130 135 140

Cura 468 SEQ list 0705

Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
 145 150 155 160
 Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
 165 170 175
 Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
 180 185 190
 Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
 195 200 205
 Arg Val Ser Arg Tyr Leu Asp Trp Ile
 210 215

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 1

<400> 98
 ctcccactcc tgctgcttct gact 24

<210> 99
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 2

<400> 99
 aaggctgggc ctaaccagct ctcac 25

<210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV7 Primer 1

<400> 100
 catgaactgg gcatttctgc agg 23

<210> 101
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV7 Primer 2

<400> 101
 ttatctgctg atctcgcagg ttatgga 27

Cura 468 SEQ list 0705

<210> 102
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 1

 <400> 102
 ctgacaggcc ctggtgtgtg at 22

 <210> 103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 2

 <400> 103
 tcacacatgt ttcattgtgg agttaga 27

 <210> 104
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 1

 <400> 104
 gagtgagagg tcggacagac tgtg 24

 <210> 105
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 2

 <400> 105
 actcatgcaa cttgcttctc tcactct 27

 <210> 106
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 1

 <400> 106
 cctatgagcc tgatgctgga tgac 24

 <210> 107

Cura 468 SEQ list 0705

<211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 2
 <400> 107
 aggactcaga ggagggagtc ctgag 25
 <210> 108
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward
 <400> 108
 gcactacaag tggaagcctt ac 22
 <210> 109
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Probe
 <400> 109
 ctcaagtaga agccgactta tgcaaa 26
 <210> 110
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag4164 Reverse
 <400> 110
 tcaaadcctt ctgagataca gt 22
 <210> 111
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward
 <400> 111
 cagctgcacg attaatgaag at 22
 <210> 112
 <211> 25

Cura 468 SEQ list 0705

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b Probe

<400> 112
 aggtcttgga ctggccttca ccatt 25

<210> 113
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

<400> 113
 ccaaagttgt gtccagactc at 22

<210> 114
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Forward

<400> 114
 ccaaggaaga cctcttcatc tt 22

<210> 115
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Probe

<400> 115
 tcttgcttac ggcataagcg ctctct 26

<210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

<400> 116
 ttcatttcta tgggacctca ga 22

<210> 117
 <211> 21
 <212> DNA
 <213> Artificial Sequence

Cura 468 SEQ list 0705

<220>
<223> Description of Artificial Sequence: Ag708 Forward

<400> 117
aaagatggga ctcgtcatga c 21

<210> 118
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Probe

<400> 118
cacgccatct tactgactgg tctgga 26

<210> 119
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Reverse

<400> 119
gtgcaaattcc caaagtgta 20

<210> 120
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Forward

<400> 120
gcactacaag tggaagcctt ac 22

<210> 121
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 121
ctcaagtaga agccgactta tgcaaa 26

<210> 122
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Reverse

Cura 468 SEQ list 0705

<400> 122
tcaaattcctt ctgcgataca gt 22

<210> 123
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 123
ccaaggaaga cctcttcatc tt 22

<210> 124
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 124
tcttgcttac ggcataagcg ctctct 26

<210> 125
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125
ttcatttcta tgggacctca ga 22

<210> 126
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 126
ccaaggaaga cctcttcatc tt 22

<210> 127
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 127
tcttgcttac ggcataagcg ctctct 26

Cura 468 SEQ list 0705

<210> 128
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

 <400> 128
 ttcatttcta tgggacctca ga 22

<210> 129
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Forward

 <400> 129
 aaagatggga ctcgtcatga c 21

<210> 130
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Probe

 <400> 130
 cacgccatct tactgactgg tctgga 26

<210> 131
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse

 <400> 131
 gtgcaaattcc caaagtgta 20

<210> 132
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward

 <400> 132
 cagctgcacg attaataag at 22

Cura 468 SEQ list 0705

<210> 133
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b Probe

 <400> 133
 aggtcttgga ctggccttca ccatt 25

 <210> 134
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

 <400> 134
 ccaaagttgt gtccagactc at 22

 <210> 135
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1537 Forward

 <400> 135
 tttcaagaca ccctgtgata cc 22

 <210> 136
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1537 Probe

 <400> 136
 acttcgtgtc ctgaatgttc caggct 26

 <210> 137
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1537 Reverse

 <400> 137
 cagaggaatg aaggcataga tg 22

 <210> 138
 <211> 21

Cura 468 SEQ list 0705

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag2432 Forward
 <400> 138
 gtaggcaaag ggactcactg t 21

<210> 139
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag2432 Probe
 <400> 139
 cagaaatcaa taatctttga ctgccg 26

<210> 140
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag2432 Reverse
 <400> 140
 gcacattacg tggctgaga 19

<210> 141
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1250 Forward
 <400> 141
 cgtggtgaac tctgccttat at 22

<210> 142
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Ag1250 Probe
 <400> 142
 cacagagctg tcgtctttga ccgatt 26

<210> 143
 <211> 21
 <212> DNA
 <213> Artificial Sequence

Cura 468 SEQ list 0705

<220>
 <223> Description of Artificial Sequence: Ag1250 Reverse
 <400> 143
 agtccctttg cctaccacaa t 21

<210> 144
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Forward
 <400> 144
 ggacccatt cgactactgt 20

<210> 145
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Probe
 <400> 145
 ctgatgacca gccgcatca atc 23

<210> 146
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Reverse
 <400> 146
 ttctcaaact gcacctggtc 20

<210> 147
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3797 Forward
 <400> 147
 tctggacgac aactattgcc 20

<210> 148
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3797 Probe

<400> 148
 atggtgctac actacggatc cgcag 25

<210> 149
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3797 Reverse

<400> 149
 gtcacagaat tctcgctcga 20

<210> 150
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2439 Forward

<400> 150
 tatcatcact tgtgatggca aa 22

<210> 151
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2439 Probe

<400> 151
 aaaaccgaga gcactttgaa aacaca 26

<210> 152
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2439 Reverse

<400> 152
 aaacttctct cccagggtac aa 22

<210> 153
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2771 Forward

<400> 153
 tgaacagaac tatgcgaaac aa 22

Cura 468 SEQ list 0705

<210> 154
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Probe

 <400> 154
 tctggttaag aagtactgcc ccaaacg 27

 <210> 155
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Reverse

 <400> 155
 ggctcttcat ctttggatga a 21

 <210> 156
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1674 Forward

 <400> 156
 ctcaactcacc acaagggagt aa 22

 <210> 157
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1674 Probe

 <400> 157
 tgacatcaaa ctcaacagtt cccagga 27

 <210> 158
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1674 Reverse

 <400> 158
 gtctaggaga gagctgagca aa 22

 <210> 159
 <211> 78

Cura 468 SEQ list 0705

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PAN domain
Consensus Sequence

<400> 159

Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu
50 55 60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys
65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin
homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln
1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His
20 25 30

Val Arg

<210> 161

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 161

Asn Glu Gln Lys
1

<210> 162

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 162

Asn His Gln Lys

1

<210> 163

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 163

Asn Asp Glu Gln

1

<210> 164

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 164

Gln His Arg Lys

1

<210> 165

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 165

Met Ile Leu Val

1

<210> 166

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Cura 468 SEQ list 0705

<400> 166

Met Ile Leu Phe
1